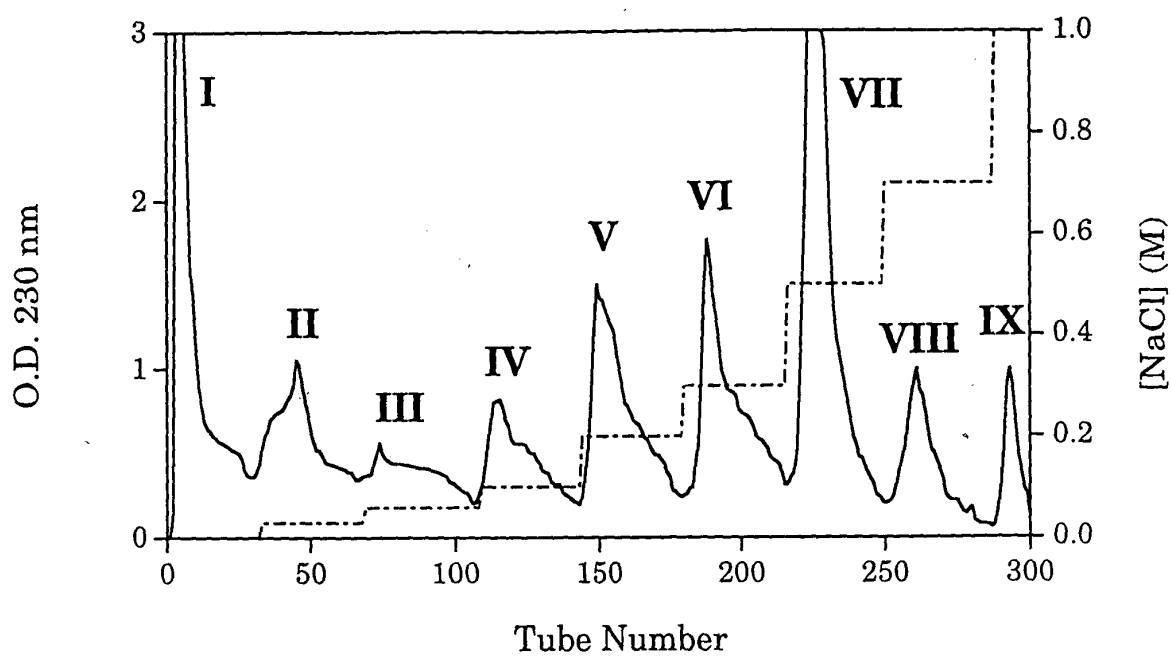


FIG 1.0

A.



B.

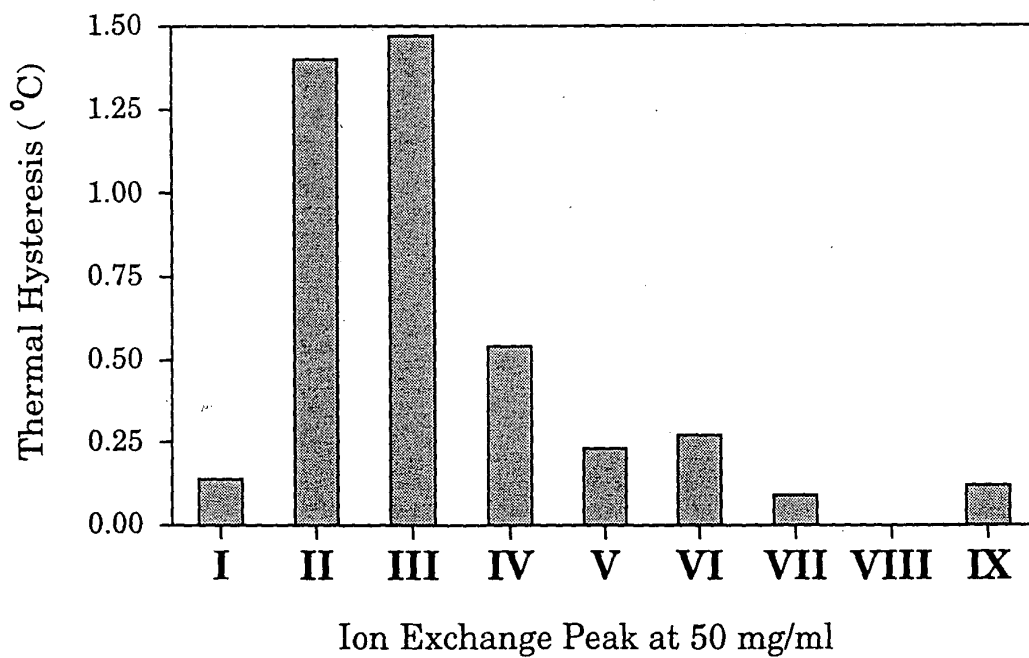


FIG 1.1

TO-090-96494860

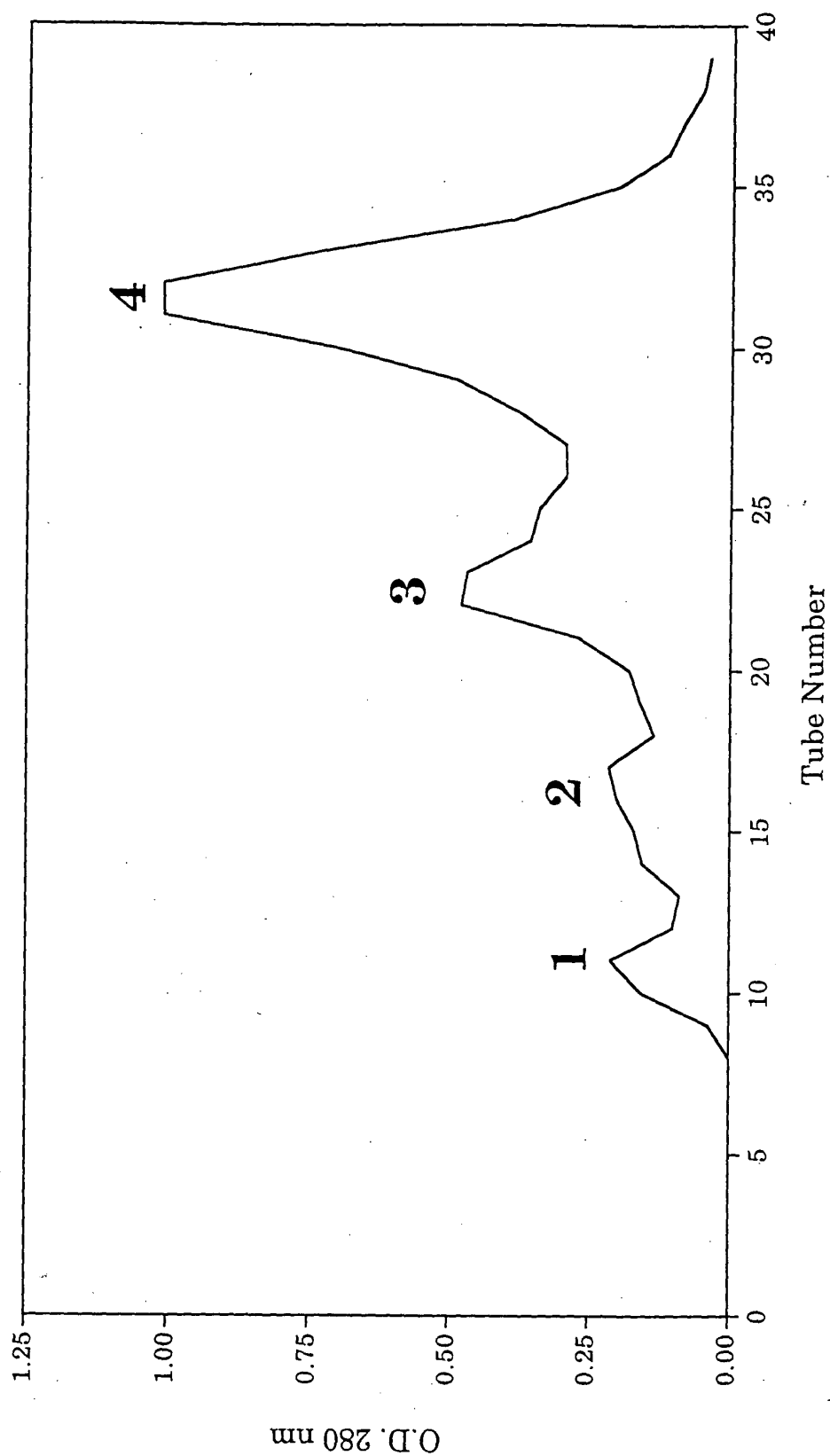


FIG 1.2

09876796.060701



FIG 1.3

Tm-12.86

12.5 25

FIG 1.4

09876796.060701

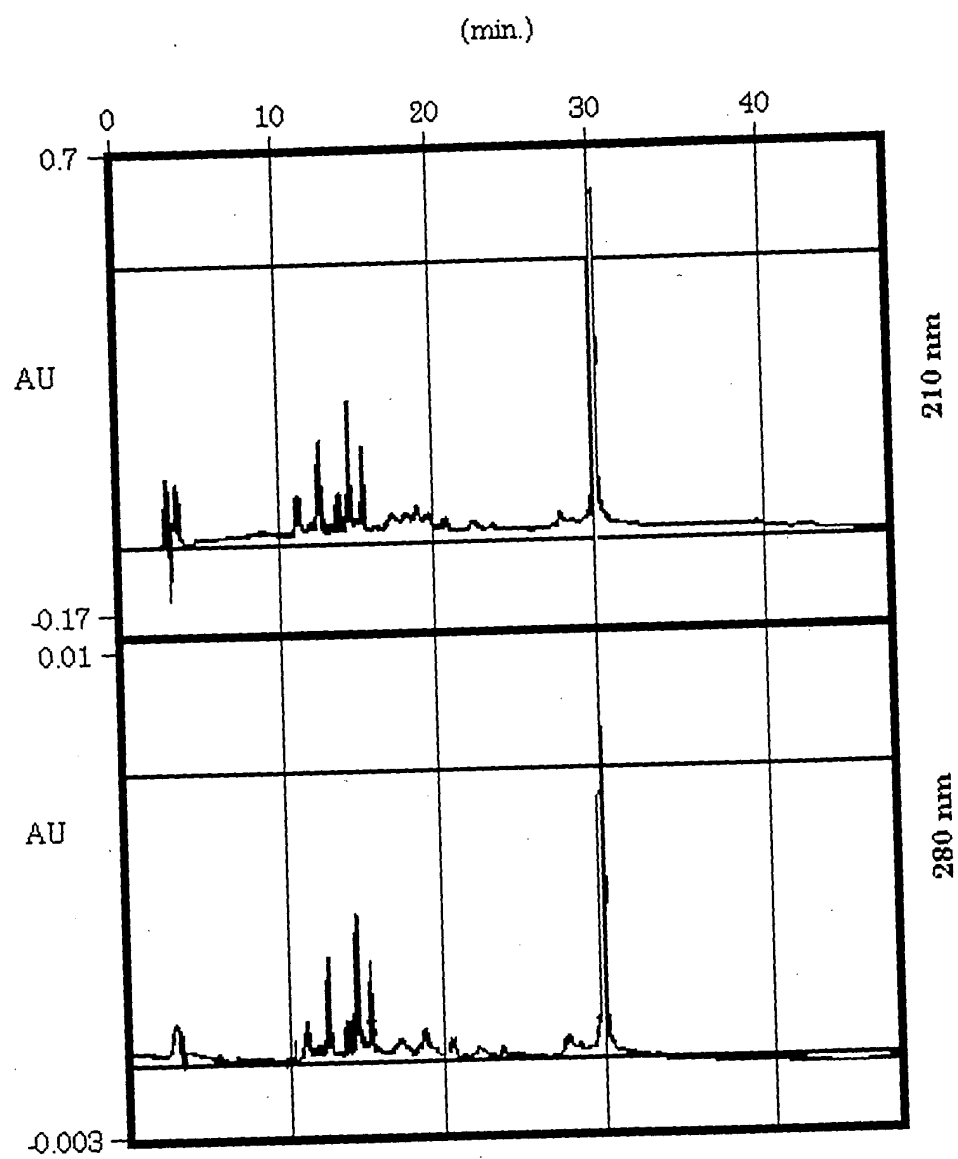


FIG 1.5

0067962860

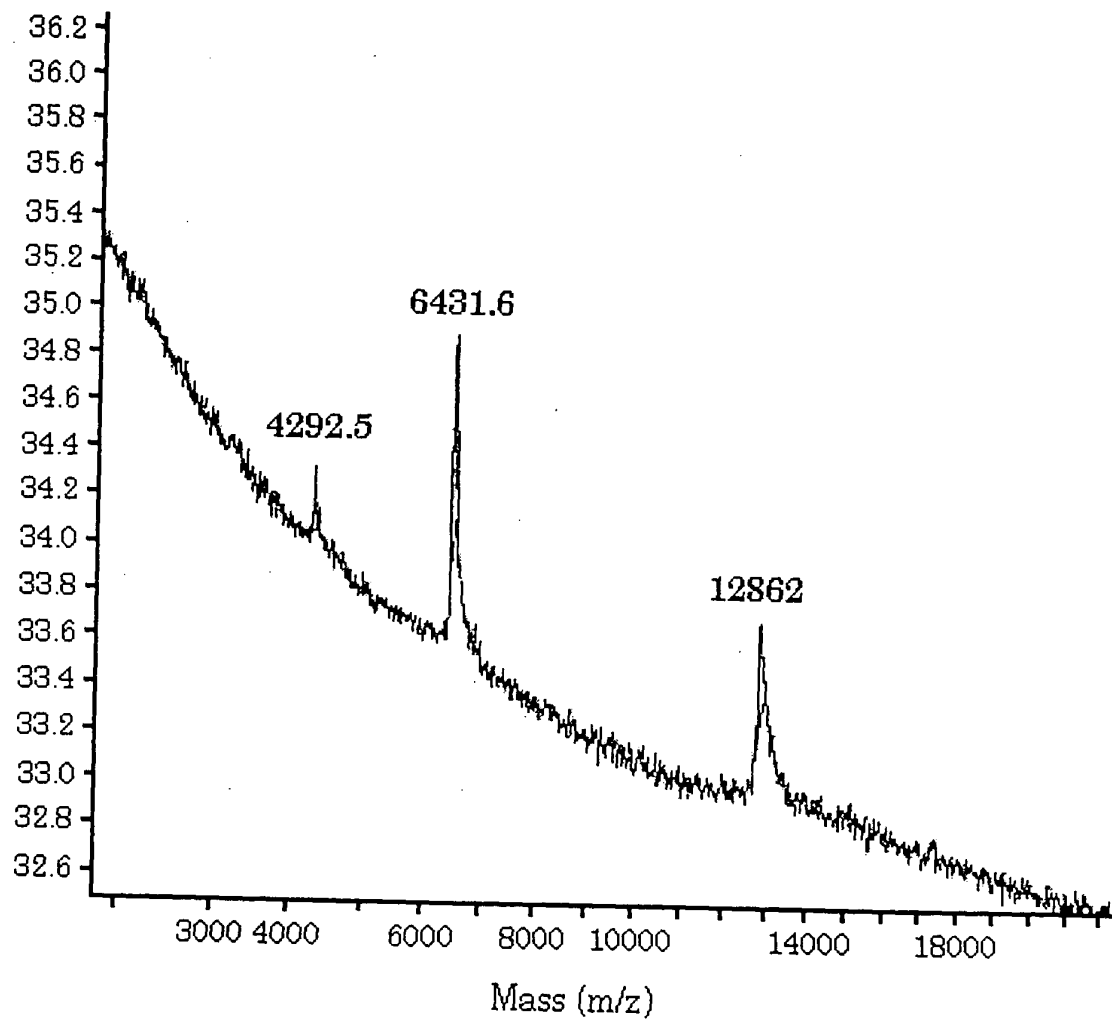


FIG 1.6



FIG 1.7

NH₂-L-T-D-E-Q-I-Q-K-R-N-K-I-S-K-E-?-Q-Q-V

Val
Gln
Gln
Glu
Lys
Ser
Ile
Lys
Asn
Arg
Lys
Gln
Ile
Gln
Asp
Thr
Leu

FIG. 1.8

[illegible]

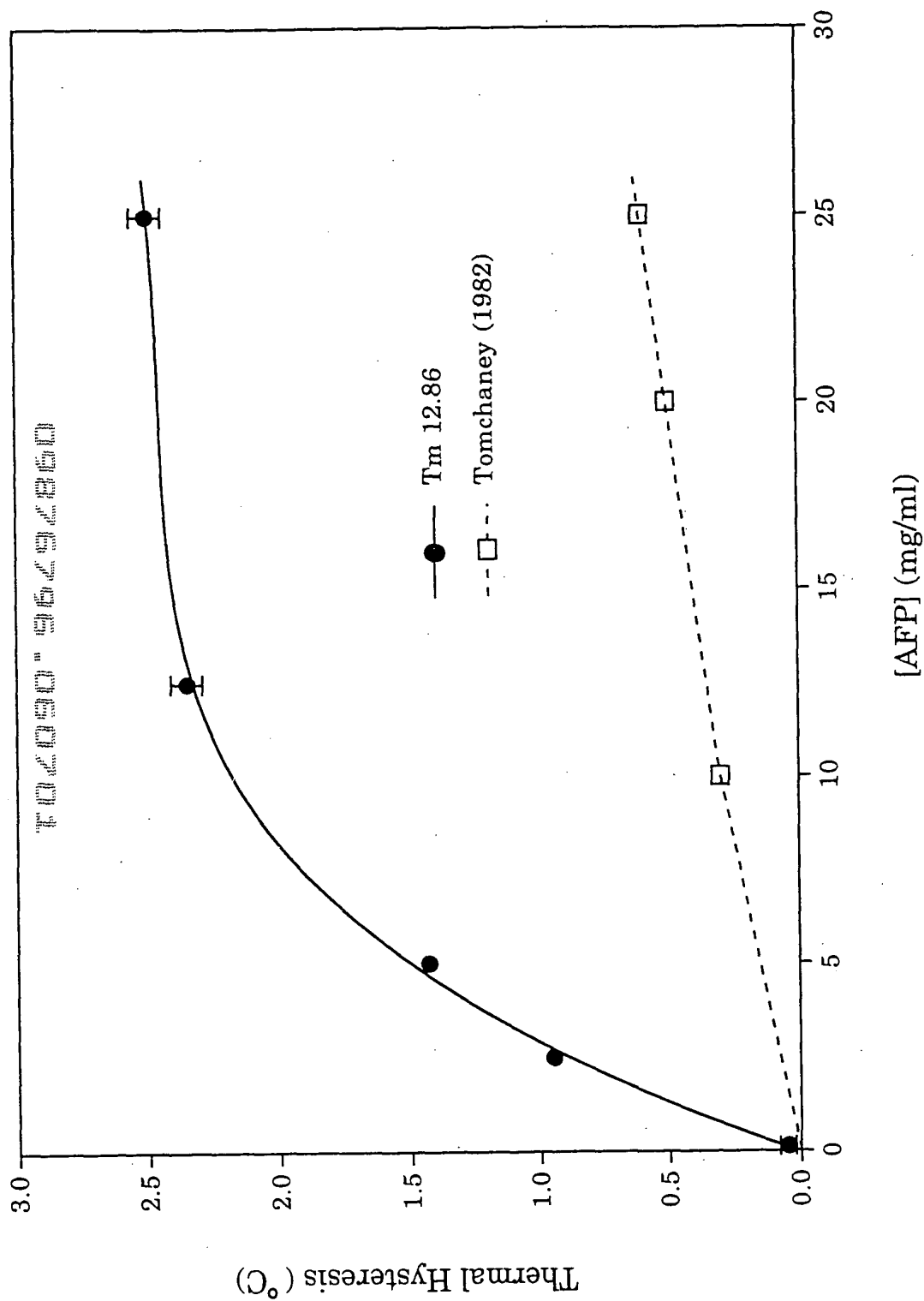


FIG 1.9

007090" 96792860

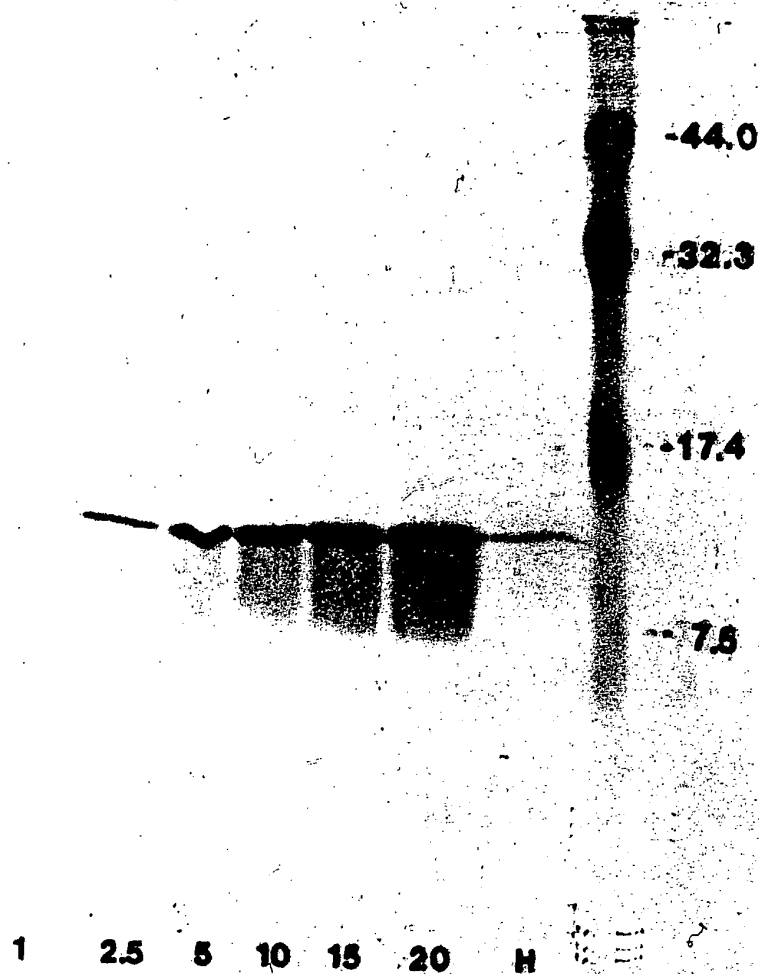


FIG 1.10

FO4090" 96292860

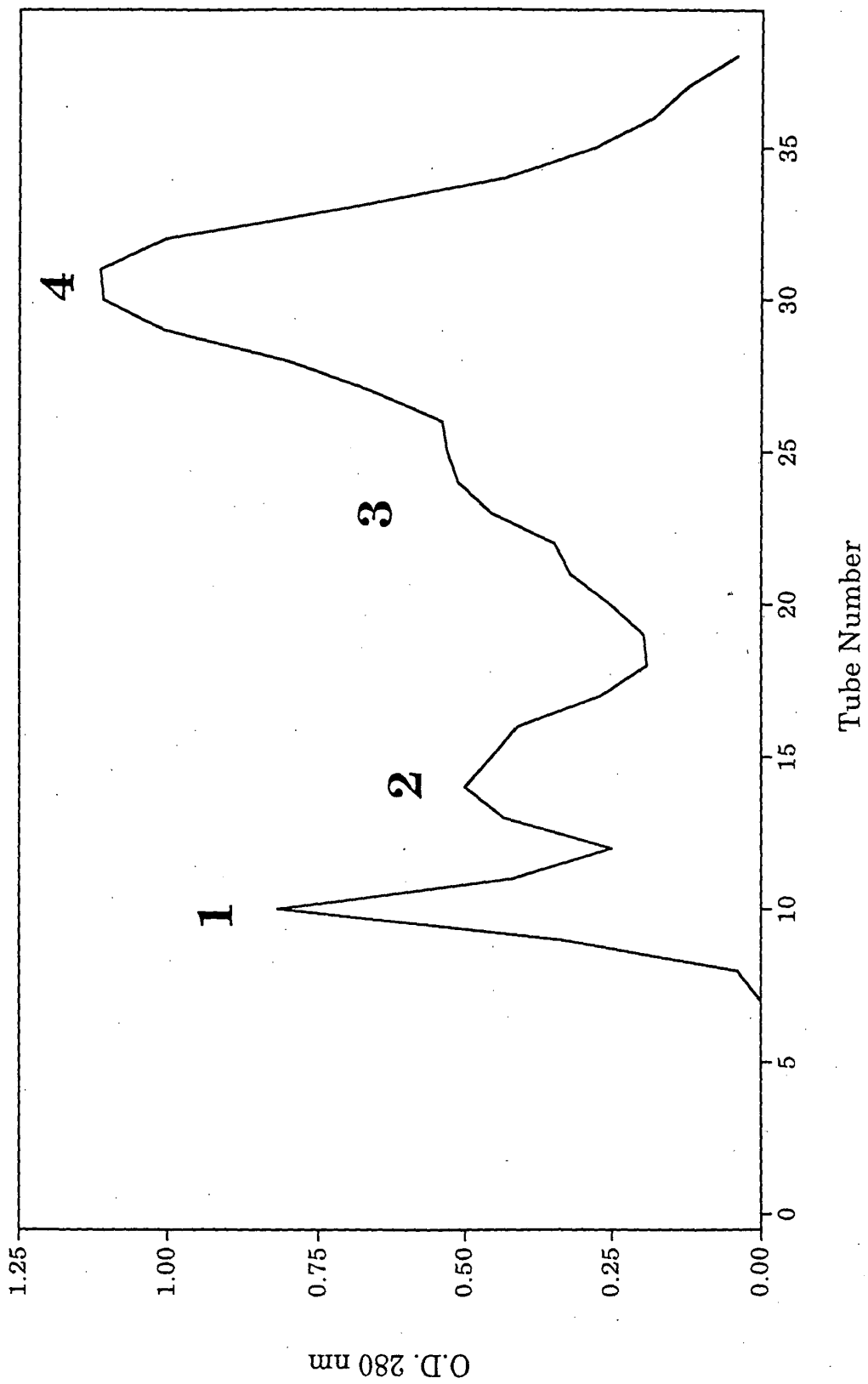


FIG 1.11

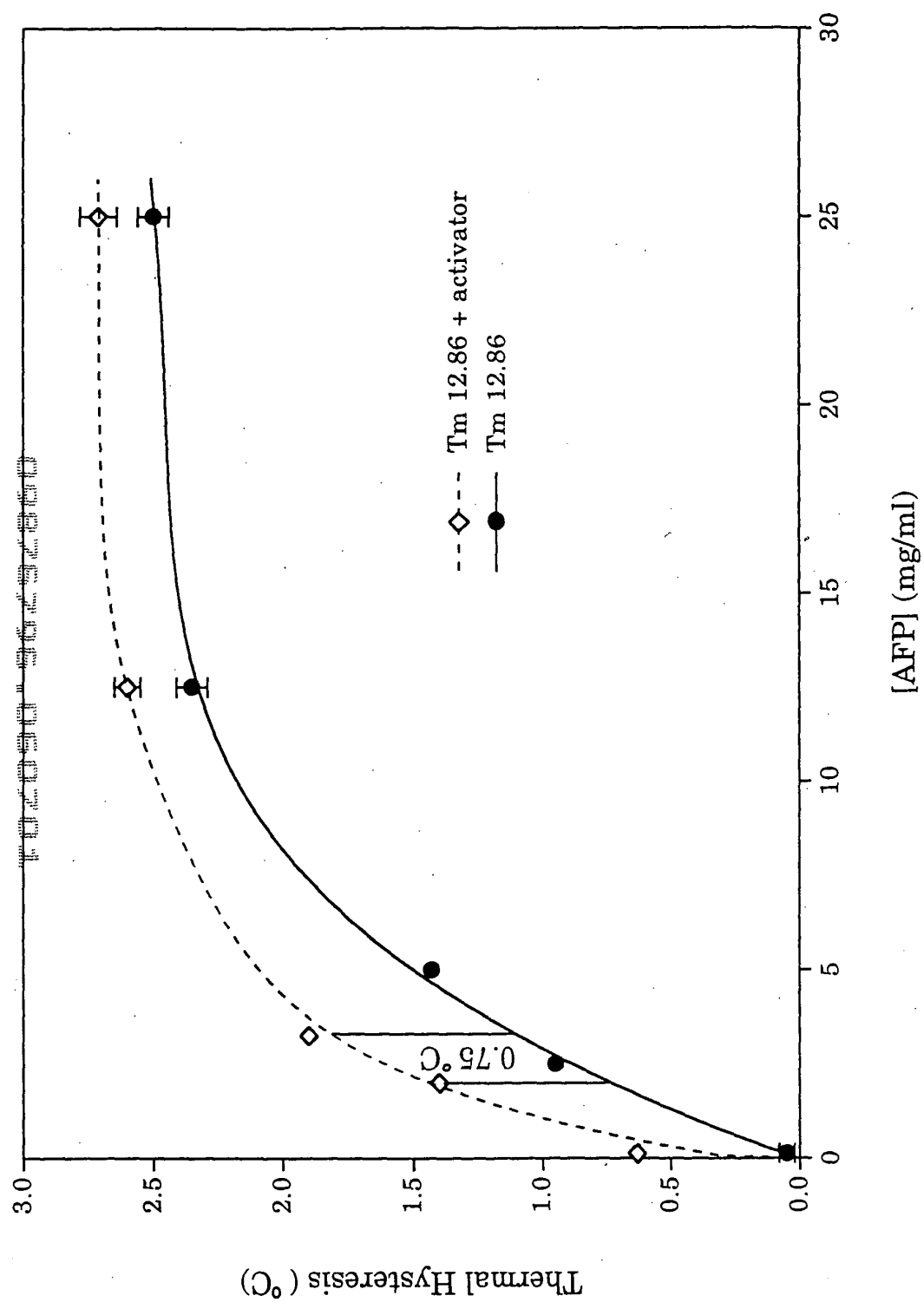


FIG 1.12

FOC030" 96797860

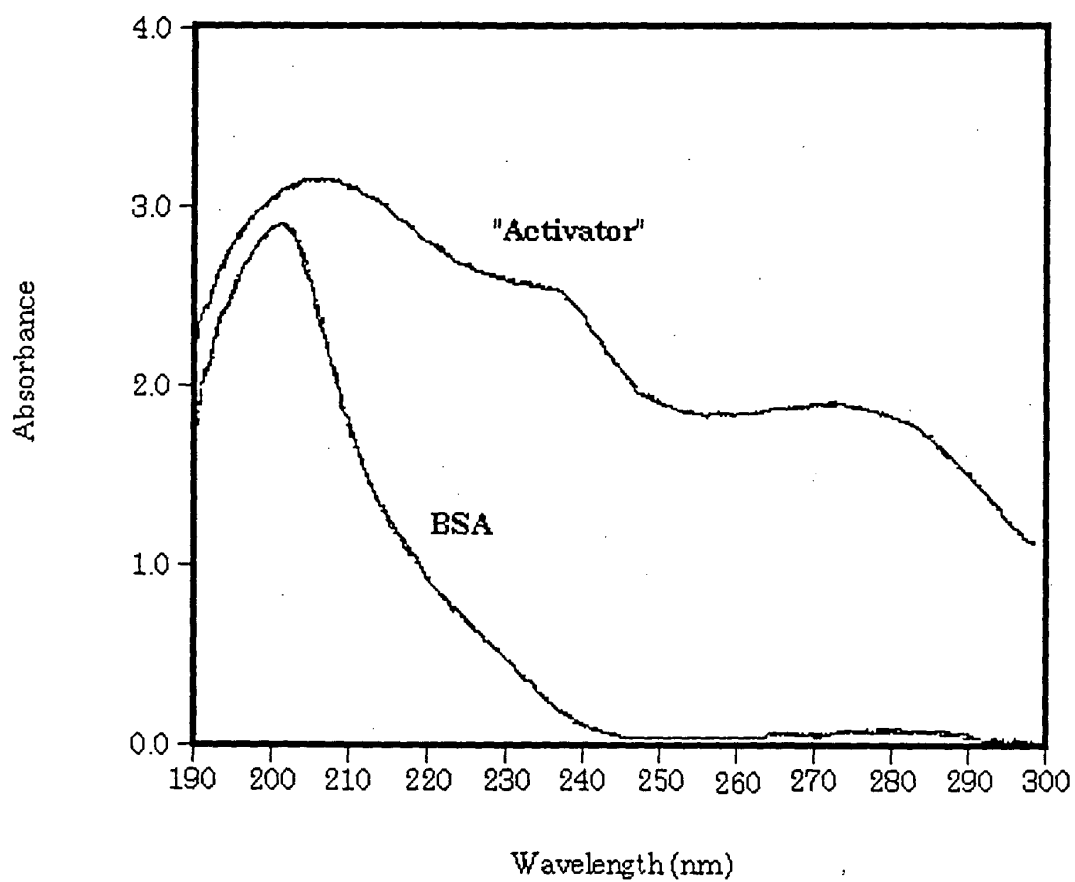


FIG 1.13

09876795-060701

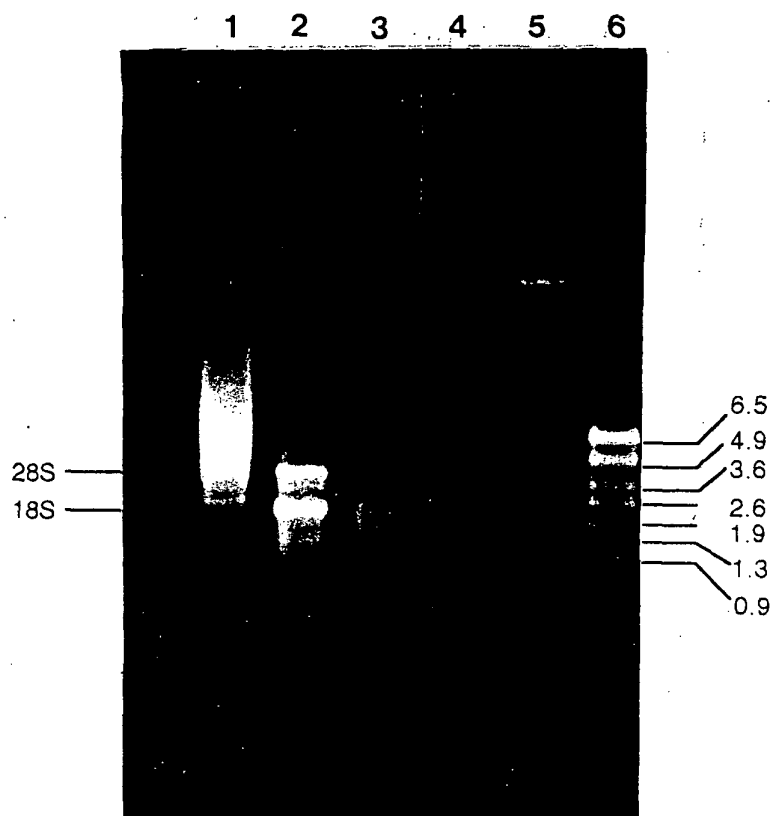


FIG 2.0

09876796.060701

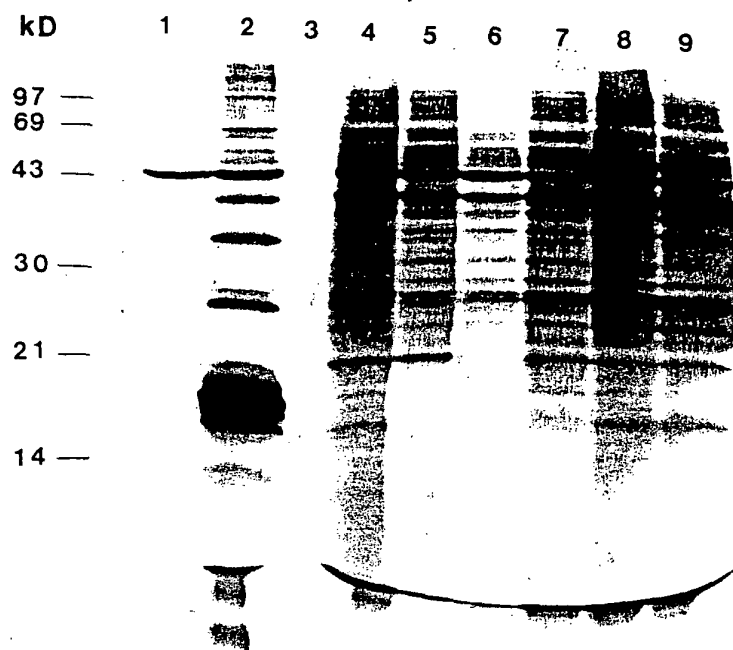


FIG 2.1

09876795050702090

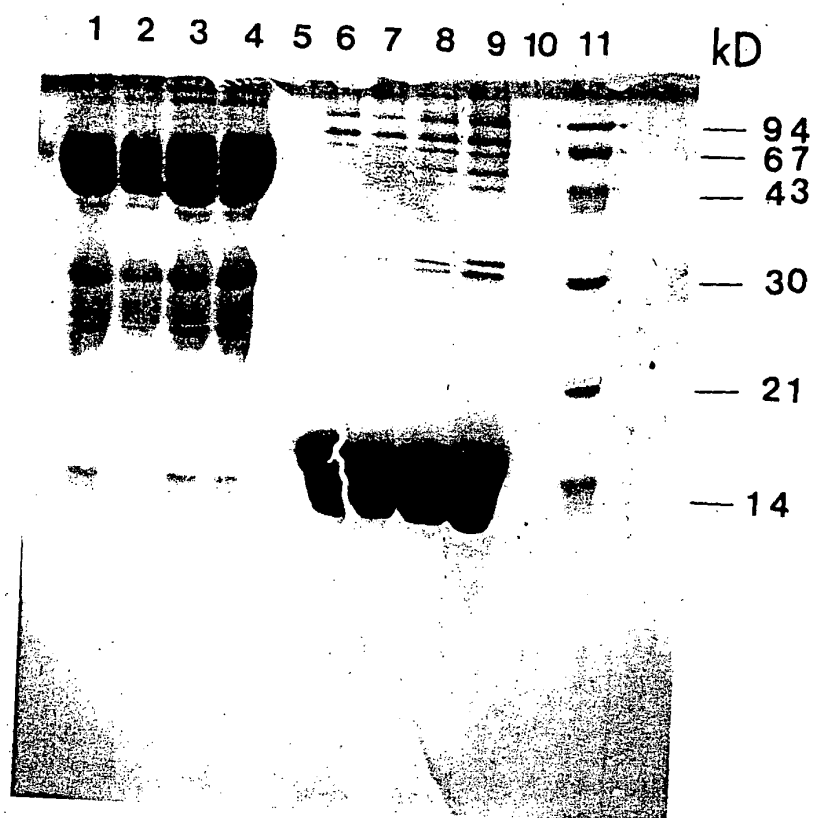


FIG 2.2

09876796-060701



FIG 2.3



五

FOUO 50292860

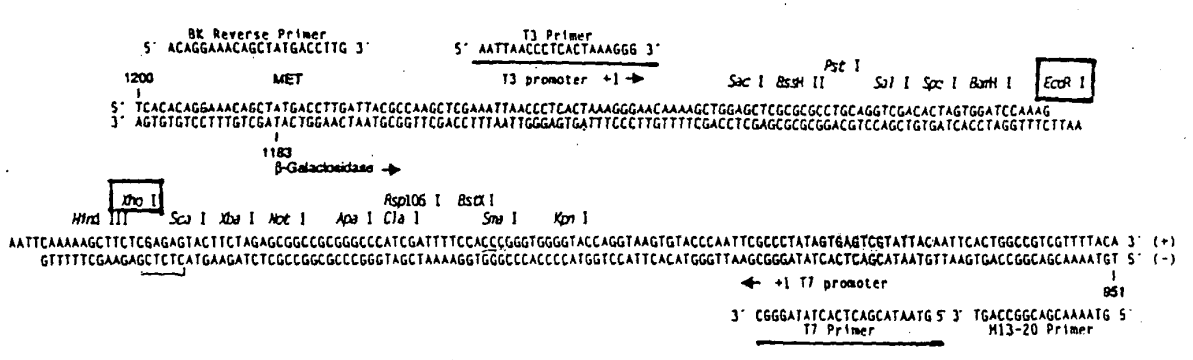
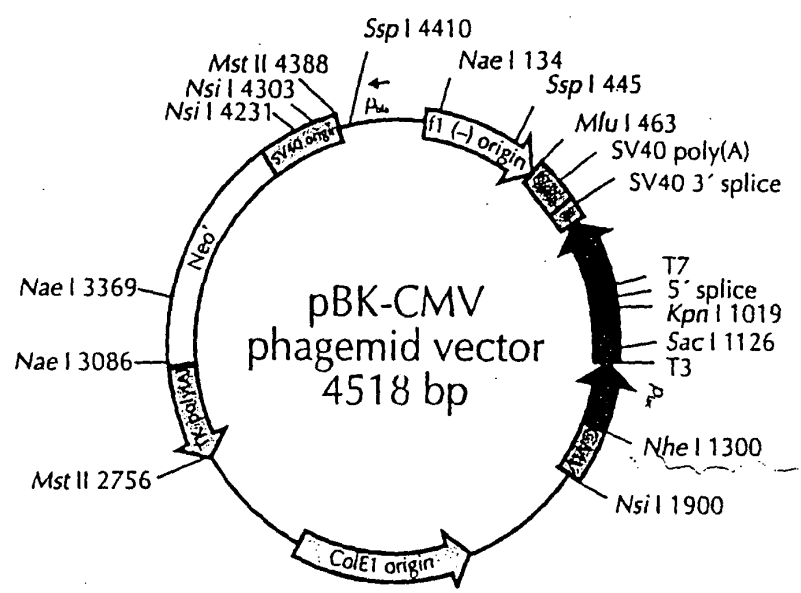


FIG. 2.4 b

FIG 2.5

DNA sequence of Tm 13.17 cDNA clone

B	E
a	C
m	O
H	R
I	I

1 AGTGGATCCAAAGAATTTCGGCACGAGACTACTAAGATCAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTCGCTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCCTCGTCAAGA
K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTCG
polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

FIG 2.6a

05876796-060701

05876795-060701

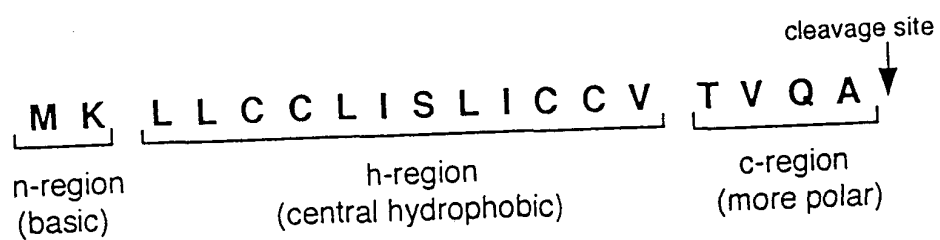


FIG 2.6b

1 LTEAQIEKLN KISKKCQNES GVSQEIIITKA RNGDWEDDPK LKRQVFCVAR
51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFEN
101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

<u>Residue</u>	<u>Number</u>	<u>Mole Percent</u>
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K =Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V =Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

FIG 2.6c

Tm 13.17 3 EAQIEKLNKISKKCQNESGVSEIITKARNGDWEDDPKLKRQVFCVARNA 52
 |.. |||.. |. |..|||:| :..|| : ||||| :..||: :..|
 AFP-3 1 ETPREKLKQHSACKAESGVSEESLNKVRNREEVDDPKLKEHAFILKRA 50

 Tm 13.17 53 GLATESGEVVVDVLREKVRKVTDNDEETEKIINKCAVKRDTVEETVFNTF 102
 |: ..|||. :| :..|...|.....| |||:| |... : |
 AFP-3 51 GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPOHSSADFF 100

 Tm 13.17 103 KCVMKKNKP 110
 ||| .|:.
 AFP-3 101 KCVHDNRS 108

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

FIG 2.8

097696-0604

FD-2090-9642860

Tm 13.17

AFP-3

B Protein

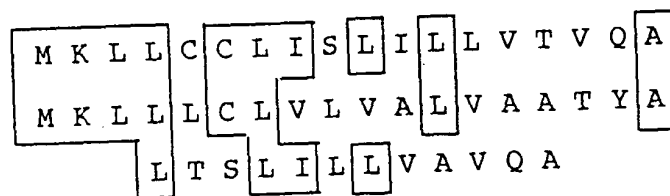


FIG 2.9

09876796-060701

Tm 13.17	NH2	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E
				:	:	:	:	:	:	:										
Tm 12.86	NH2	L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V

FIG 2.10

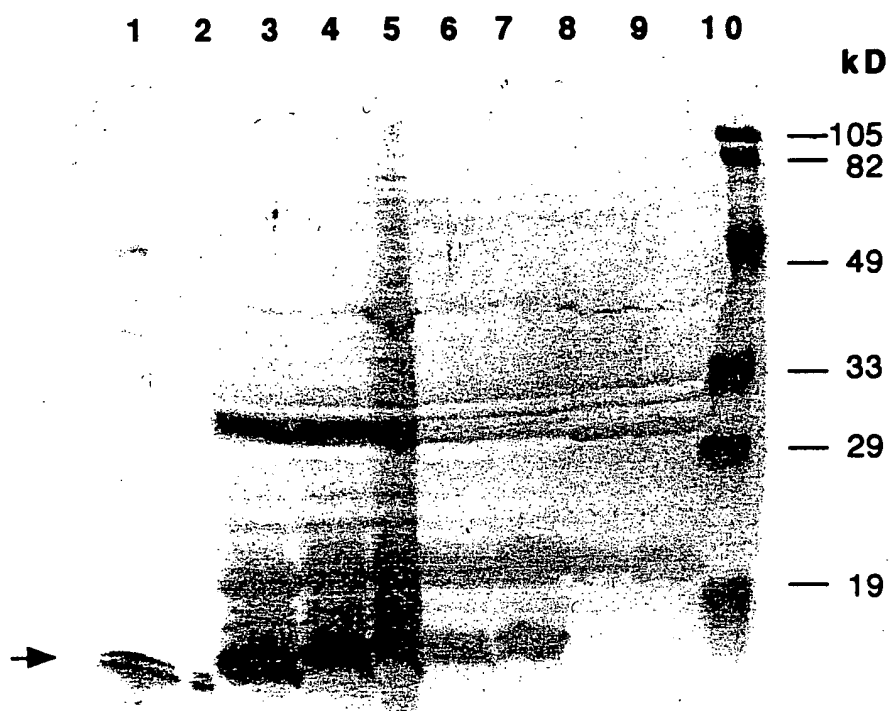


FIG 2.11

Tm 12.86		L	T	D	E	Q	I	Q	K	R	N	K	I	S	K	E	?	Q	Q	V												
Tm 13.17	1	L	T	E	A	Q	I	E	K	L	N	K	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	A	30
B1	13	I	T	E	E	D	L	E	L	L	R	Q	T	S	A	E	C	K	T	E	S	G	V	S	E	D	V	I	K	R	A	43
AFP-3	1		E	T	P	R	E	K	L	K	Q	H	S	D	A	C	K	A	E	S	G	V	S	E	E	S	L	N	K	V	28	
Tm13.17	31	R	N	G	D	W	E	D	D	P	K	L	K	R	Q	V	F	C	V	A	R	N	A	G	L	A	T	E	S	G	E	60
B1	44	R	K	G	D	L	E	D	D	P	K	L	K	M	Q	L	L	C	I	F	K	A	L	E	I	V	A	E	S	G	E	74
AFP-3	29	R	N	R	E	E	V	D	D	P	K	L	K	E	H	A	F	C	I	L	K	R	A	G	F	I	D	A	S	G	E	58
Tm13.17	61	V	V	V	D	V	L	R	E	K	V	R	K	V	T	D	N	D	E	E	T	E	K	I	I	N	K	C	A	V	K	90
B1	75	I	E	A	D	T	F	K	E	K	L	T	R	V	T	N	D	D	E	E	S	E	K	I	V	E	K	C	T	V	T	105
AFP-3	59	F	Q	L	D	H	I	K	T	K	F	K	E	N	S	E	H	P	E	K	V	D	D	L	V	A	K	C	A	V	K	88
Tm13.17	91	R	D	T	V	E	E	T	V	F	N	T	F	K	C	V	M	K	N	K	P	K	F	S	P	V	D					116
B1	106	E	D	T	P	E	D	T	A	F	E	V	T	K	C	V	L	K	D	K	P	N	F	F	G	D	L	F	V			124
AFP-3	89	K	D	T	P	Q	H	S	S	A	D	F	F	K	C	V	H	D	N	R	S											108

FIG 2.12

T02090" 96292360

```

1   GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
      M   K   L   L   L   C   F   A   F   A   A
47  ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
      I   V   I   G   A   Q   A   L   T   D   E   Q   I   Q   K
      ↑
92  AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
      R   N   K   I   S   K   E   C   Q   Q   V   S   G   V   S
137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
      Q   E   T   I   D   K   V   R   T   G   V   L   V   D   D
182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
      P   K   M   K   K   H   V   L   C   F   S   K   K   T   G
226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
      V   A   T   E   A   G   D   T   N   V   E   V   L   K   A
271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
      K   L   K   H   V   A   S   D   E   E   V   D   K   I   V
316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
      Q   K   C   V   V   K   K   A   T   P   E   E   T   A   Y
361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCT
      D   T   F   K   C   I   Y   D   S   K   P   D   F   S   P
406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
      I   D   *
                                     polyadenylation signal
451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

```

poly (A) tail

FIG 3.0

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K C I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D * polyadenylation signal

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

poly (A) tail

FIG 3.1

start



2-2	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C	G
2-3	G G C A C G A G C A A A A A T G A A A C T C C T C T T G T G C T T T G C	T
2-2	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G	
2-3	T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G	
2-2	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A	
2-3	A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A	
2-2	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C	
2-3	A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C	
2-2	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A	T G A T C C C A
2-3	G A C A A A G T C C G C A C A G G T G T C T T G G T C G A	C G A T C C C A
2-2	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C	
2-3	A A A T G A A G A A G C A C G T C C T C T G C T T C T C G A A G A A A A C	
2-2	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G	
2-3	T G G A G T G G C A A C C G A A G C C G G A G A C A C C A A T G T G G A G	
2-2	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G	
2-3	G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G	
2-2	A A G A	G G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-3	A A G A	A G T G G A C A A G A T C G T G C A G A A G T G C G T G G T C A A
2-2	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C	
2-3	G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C	
2-2	A A G T G T A T T T A C G A C A G	C A A A C C T G A T T T C T C T C C T A
2-3	A A G T G T A T T T A C G A C A G	T A A A C C T G A T T T C T C T C C T A
2-2	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A	
2-3	T T G A T T A A T T G T T T T G T A T T T G A C T G A A T T T T G A C A A	
2-2	T A A A G G T A	A T A T C G T T A T G T A A A A A
2-3	T A A A G G T A	C T A T C G T T A T G A A A A A

FIG 3.2

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG 3.3

102090" 36292860

09876796.060704

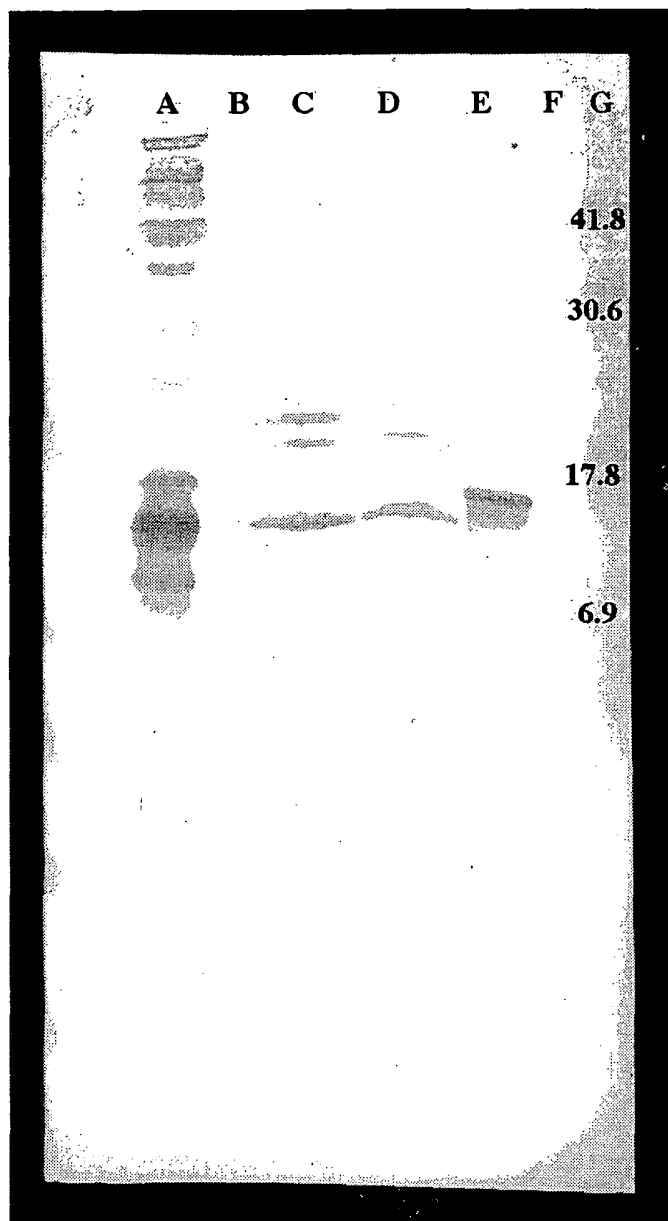


FIG 3.4

09876796-060701

Lane

1 2 3 4 5

a → ← a
b → ← b

577 bp

483 bp

FIG 4.0

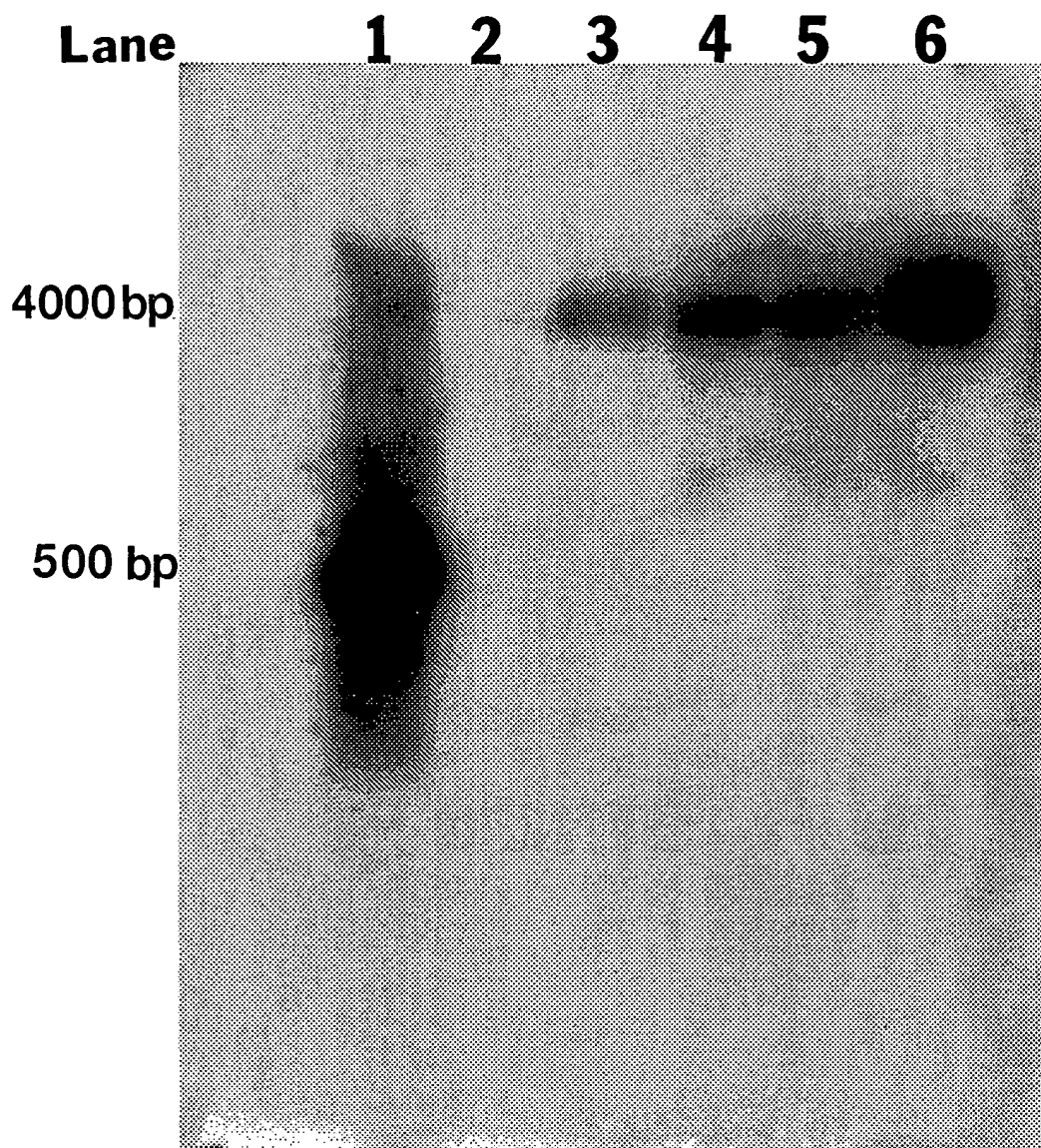


FIG 4.1

09876796.080701

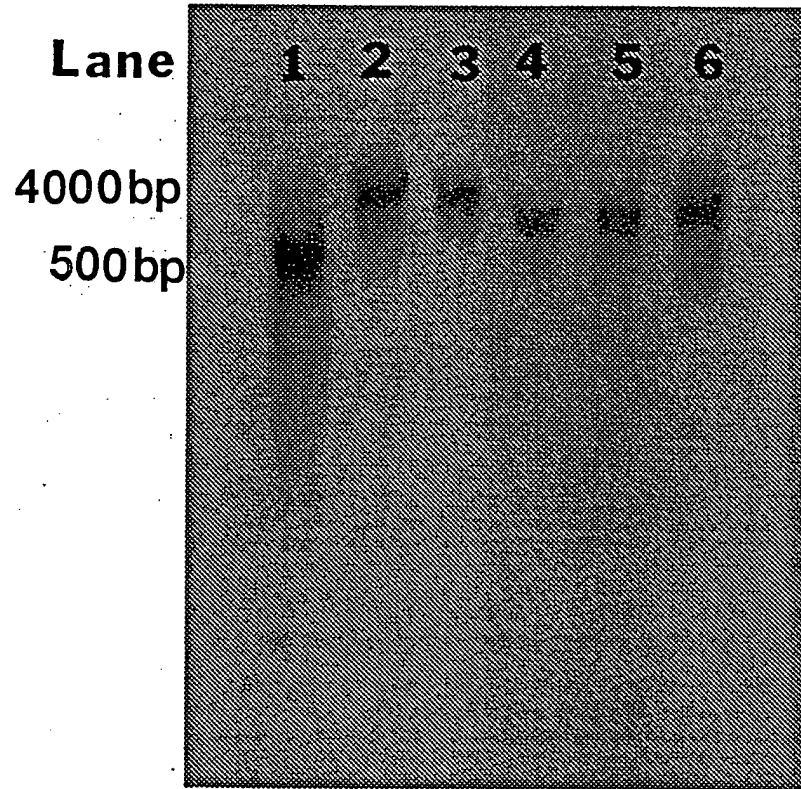


FIG 4.2

TD4090" 96292860

A.

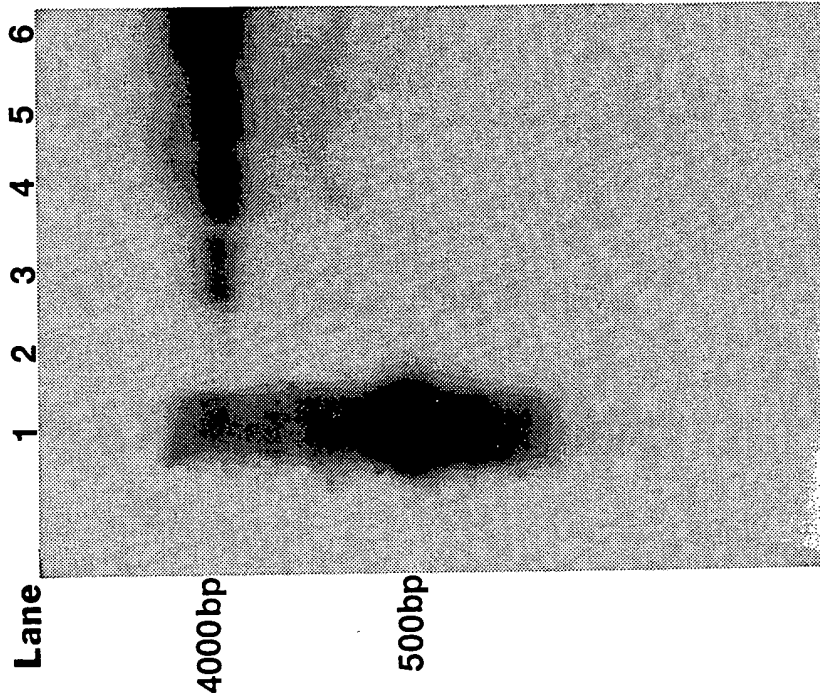
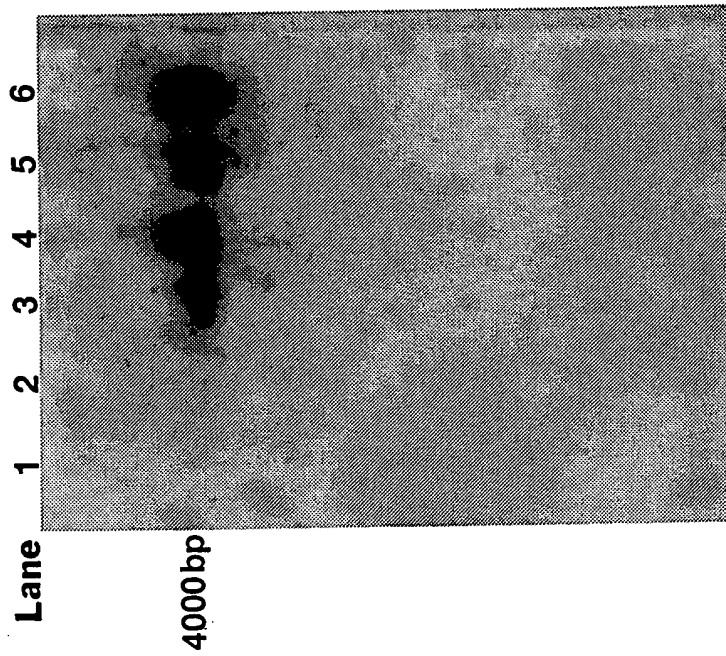


FIG 4.3

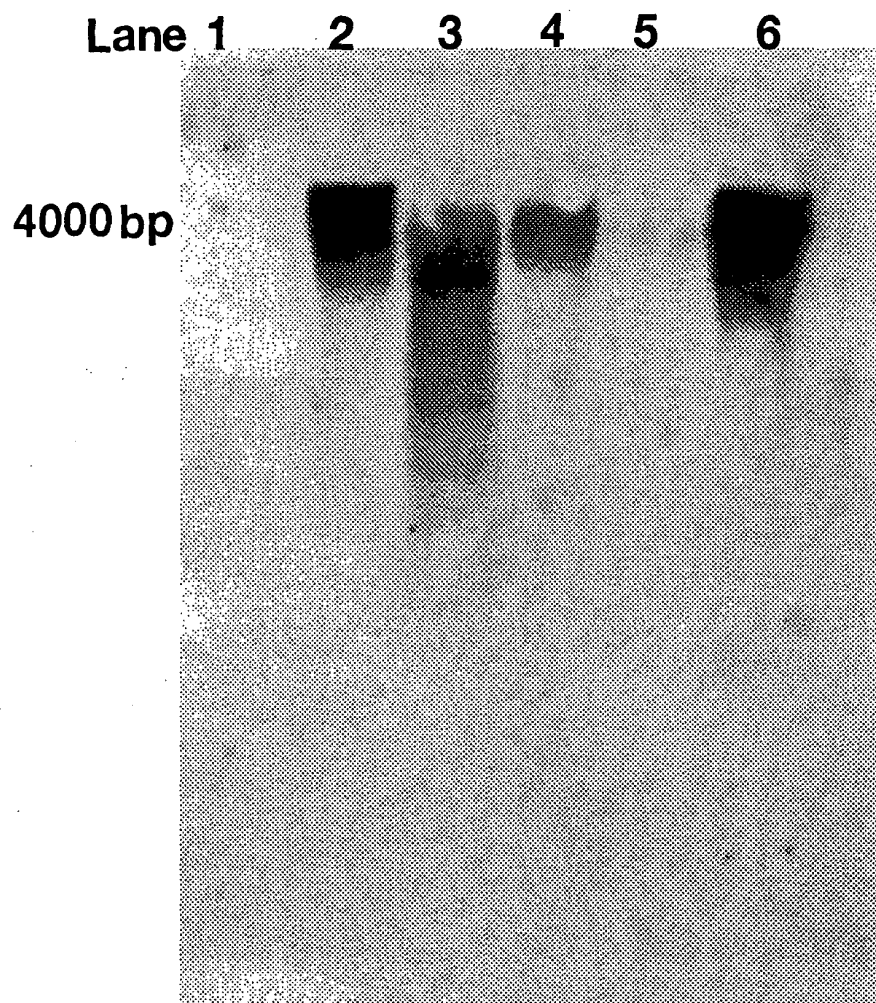
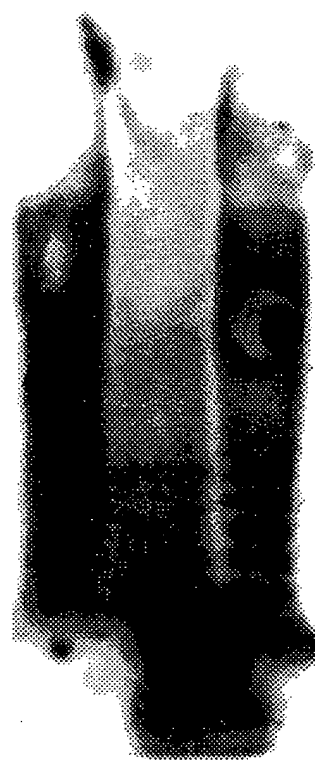


FIG 4.4

09876796-060701

09676796-060701

Lane 1 2 3 4 5



23130

9416

4361

2322
2027

564

FIG 4.5

Tm 13.17 cDNA

1 AGTGGATCCAAAGAATTCGGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
L I L L V T V Q A L T E A Q I E K L N K
↑ Forward Primer

121 AGATCAGCAAAAAATGTCAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTTCGACGTGTTGAGGGAGAAGGTGA
A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
K V T D N D E E T E K I I N K C A V K R
Reverse Primer

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
D T V E E T V F N T F K C V M K N K P K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
F S P V D *

481 ATATAAAAAATAAAGTGTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAAAACTC

FIG. 4.6 a

B.

Forward Primer

2-2 LTDEQIQKRNKISKECQQVS **GVSQET** IDKVRTGVLV
 Tm 13.17 LTEAQIEKLNKISKKQNES **GVSQEI** ITKARNGDWE
 B2 LTEEDLQLLRQTSAECKTES **GASEA** VIKKARKGDLE
 AFP-3 ETPREKLKQHSDACKAES **GVSEES** LNKVRNREEV

2-2 DDPKMKKHVLCFSSKKTGVATEAGDTNVEVLKAKLKH
 Tm 13.17 DDPKLKRQVFCVARNAGLATESGEVVVDVLRKVRK
 B2 DDPKLKMQLLCIFKALEIVAESGEIEADTFKEKLTR
 AFP-3 DDPKLKEHAFCLKRAGFIDASGEFQLDHIKTKFKE

Reverse Primer

2-2 VAS DEEVDKIVQKCVVKK **ATPEET** AYDTFKCIYDS
 Tm 13.17 VTDNDEETEKIINKCAVKR **DTVEET** VFNTFKCVMKN
 B2 VTNDDEESEKIVEKCTVTE **DTPEDT** AFEVTKCVLKD
 AFP-3 NSEHPEKVDDLVAKCAVKK **DT PQHS** SADFFKCVHDN

2-2 KPDFSPI D
 Tm 13.17 KPKFSPVD
 B2 KPNFFGDLFV
 AFP-3 RS

percent % composition

Primer A C G T Melting Temperature(°C)

Forward	28.6	14.3	42.9	14.3	44.0
Reverse	25.0	31.3	6.3	37.5	44.0

FIG 4.6

T.D.2050-95/96-050701

C.

09876796-060701

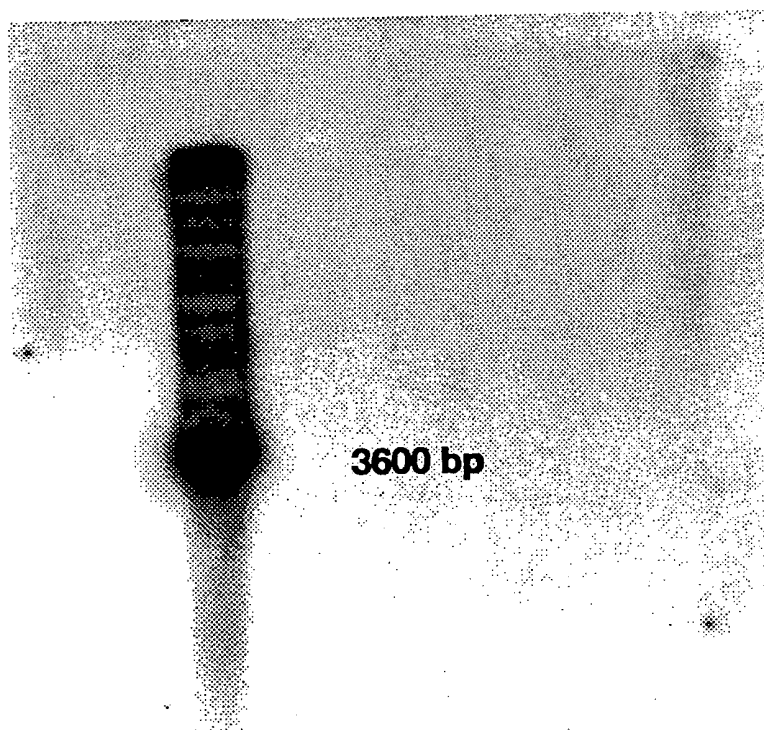


FIG 4.7

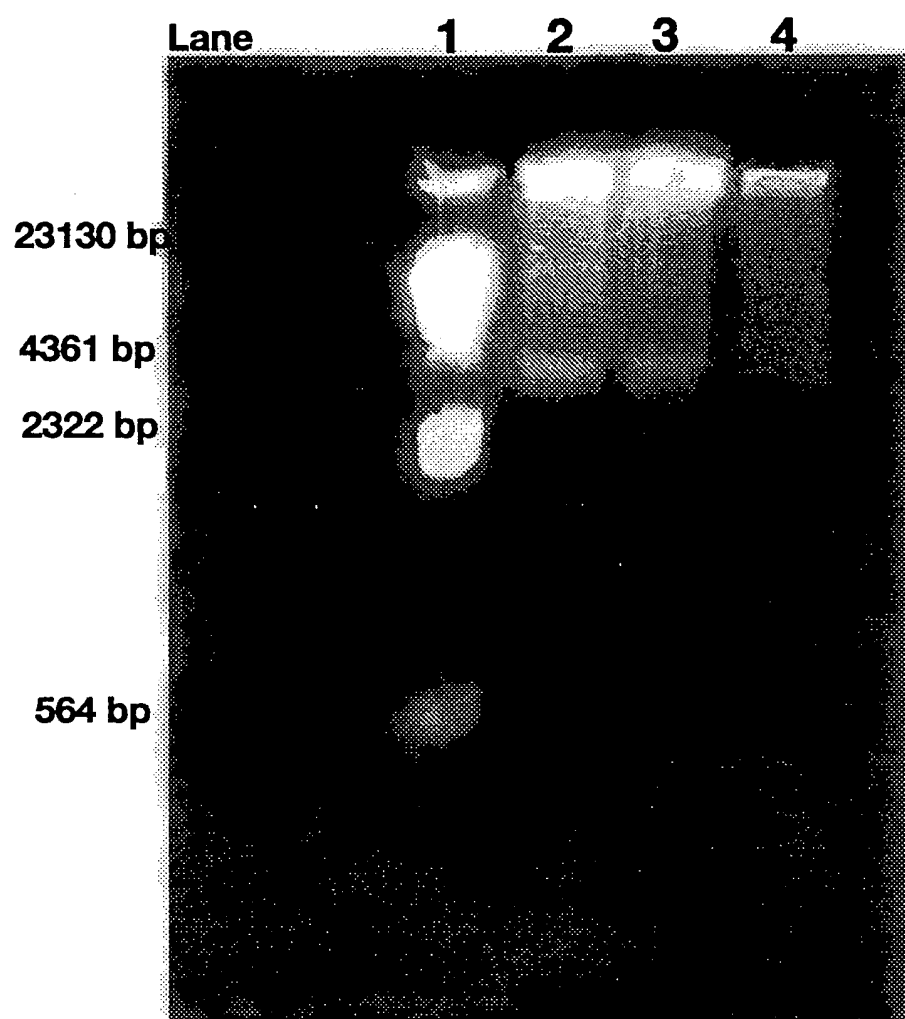


FIG 4.8

09876795-060701

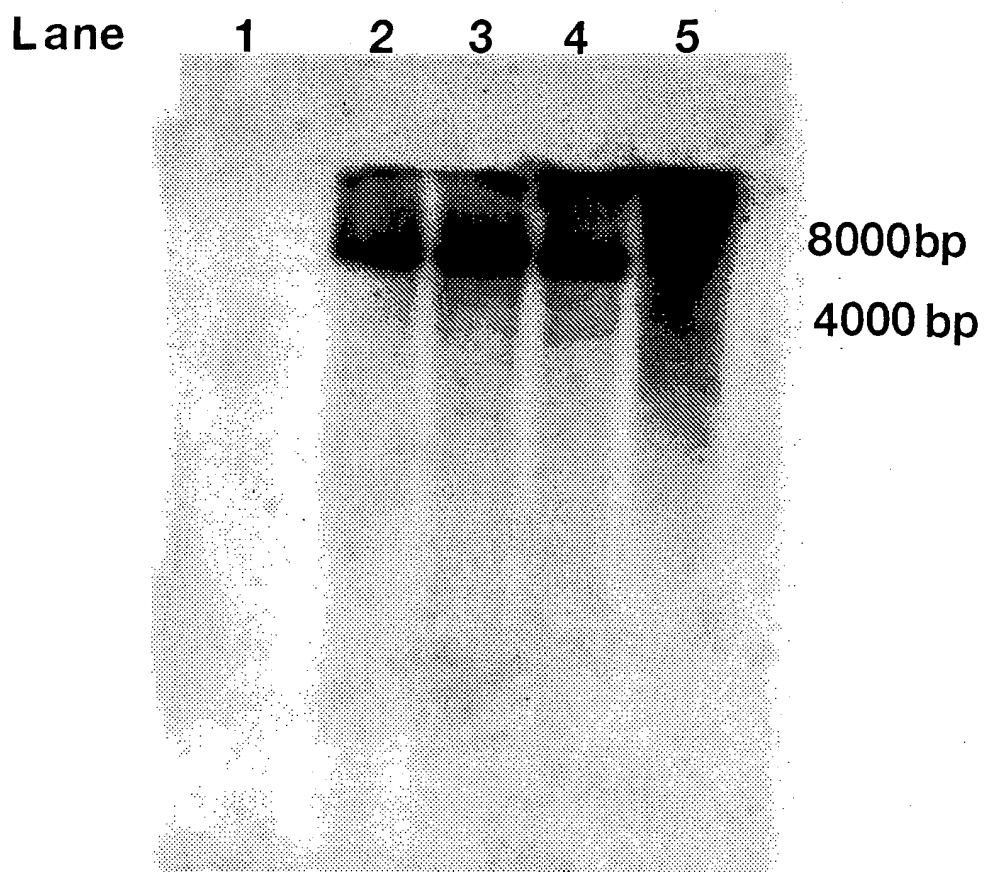


FIG 4.9

1 GGCACGAGCAAAAATGAAACTCCTCTTGTGCTTTGCTTTGCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGGTTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAA polyadenylation signal

poly (A) tail

FIG. 4.10 a

Analysis	Whole Protein
Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Predicted Amino Acid

Composition of 3-4

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.10 b

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCTTTGCGCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGATGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGAGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAGAACTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

FIG. 4.11 a

T02090-96292850

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
I Ile	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
T Thr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
Ter	0	0.00	0.00

FIG. 4.11 b

T02090" 916292860

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAGTGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q E S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGACGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K R T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAAGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGTAAACCTGATTTCTCTCCT
D T F K V I Y D S K P D F S P

406 ATTGATTAATTGTTTTGTATTTGGCTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAA

polyadenylation signal

poly (A) tail

FIG. 4.12 a

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

Amino Acid(s)	Number count	% by weight	% by frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I Ile	6	5.29	5.22
K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

FIG. 4.12 b

T02090" 96292850



G T A A A A A A A A A A A A A A A A

FIG. 4.13

FD-302 (Rev. 3-7-60)



2-2 MKLLLLCFAFAAIVIGAQAALTDEQIQKRNKISKECQQQVSGVSSQETIDKVRTGVLV
2-3 MKLLLLCFAFAAIVIGAQAALTDEQIQKRNKISKECQQQVSGVSSQETIDKVRTGVLV
3-4 MKLLLLCFAFAAIVIGAQAALTDEQIQKRNKISKECQQQVSGVSSQETIDKVRTGVLV
3-9 MKLLLLCFAFAAIVIGAQAALTDEQIQKRNKISKECQQQVSGVSSQETIDKVRTGVLV
7-5 MKLLLLCFAFAAIVIGAQAALTDEQIQKRNKISKECQQQVSGVSSQETIDKVRTGVLV

2-2 DDPKMKKHHVLCFSSKKTGVA TEAGDTNVEVLKAKLKHVAASDEEEVDKIVQKCVVKK
2-3 DDPKMKKHHVLCFSSKKTGVA TEAGDTNVEVLKAKLKHVAASDEEEVDKIVQKCVVKK
3-4 DDPKMKKHHVLCFSSKKTGVA TEAGDTNVEVLKAKLKHVAASDEEEVDKIVQKCVVKK
3-9 DDPKMKKHHVLCFSSKKTGVA TEAGDTNVEVLKAKLKHVAASDEEEVDKIVQKCVVKK
7-5 DDPKMKKHHVLCFSSKKTGVA TEAGDTNVEVLKAKLKHVAASDEEEVDKIVQKCVVKK

2-2 ATPEETAYDTFKCIYDSKPPDFSPI D*
2-3 ATPEETAYDTFKCIYDSKPPDFSPI D*
3-4 ATPEETAYDTFKCIYDSKPPDFSPI D*
3-9 ATPEETAYDTFKCIYDSKPPDFSPI D*
7-5 ATPEETAYDTFKCIYDSKPPDFSPI D*

FIG. 4.14

	(kDa)	(% mole)																	% most hydrophilic			
		MW	AA	Cys	Pro	Phe	Ile	Val	Met	Leu	% most hydrophobic	Gly	Ala	Tyr	His	Trp	Asx	Glx		Arg	Lys	Ser
Tm 12.86	12.86	117	3.2	3.0	3.4	4.4	8.5	2.0	4.4	28.9	3.1	3.9	3.8	3.2	ND	10.7	15.0	3.6	14.9	6.8	6.3	57.3
	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24	0	0	1.4	0	0	7.12	15.6	3.31	6.14	32.14
Tm 13.17	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
3-4	12.84	115	2.41	3.02	3.44	5.29	11.6	1.02	4.41	28.04	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.09	32.24
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77	3.31	2.54	2.13	0	0	0	3.64	16.9	4.74	7.07	32.38
7-5	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02	4.41	27.26	1.78	3.32	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23

FIG. 4.15

NUCLEONIDE SEQUENCES

PERCENT SIMILARITY

		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1		99.1	97.3	98.4	98.2	50.4	42	42.4	20.7	20.9	1	2-2
	2	0.9		99	99	99	51.5	43.2	42.7	20.2	21.3	2	2-3
	3	1.6	60		98	98	50.3	42	42.1	20	20	3	3-4
	4	1.6	20	80		98.4	51.3	43.7	43.6	20.4	22	4	3-9
	5	1.8	25	75	45		50.4	42.5	42.9	22.2	23.1	5	7-5
	6	36.9	36.4	37.2	36.4	37.1		57.2	37.4	23.3	21	6	Tm 13.17
	7	39.9	41.2	41.7	40.7	41.2	30.2		39.3	21.9	22.1	7	B1
	8	41.8	42.4	43.1	42.3	42.3	45.3	49.4		21.8	23.1	8	AFP-3
	9	48.7	58.6	52	51.2	51.9	61.7	62.2	58.2		45.6	9	YL-1
	10	51.4	62.7	46.4	46.5	46.5	60	58.1	61.8	35.5		10	DAFP-1A
		1	2	3	4	5	6	7	8	9	10		

AMINO ACID SEQUENCES

PERCENT SIMILARITY

		1 ²⁻²	2 ²⁻³	3 ³⁻⁴	4 ³⁻⁹	5 ⁷⁻⁵	6 ^{Tm13.17}	7 ^{B1}	8 ^{AFP-3}	9 ^{YL-1}	10 ^{DAFP-1A}		
PERCENT DIVERGENCE	1		100	99.1	99.1	100	51.3	37.4	35.2	11.6	12	1	2-2
	2	0		99.1	99.1	100	51.3	37.4	35.2	11.6	12	2	2-3
	3	0.9	0.9		98.3	99.1	50.4	36.5	34.3	11.6	12	3	3-4
	4	0.9	0.9	1.7		99.1	51.3	37.4	36.1	10.7	12	4	3-9
	5	0	0	0.9	0.09		51.3	37.4	35.2	11.6	12	5	7-5
	6	46.1	46.1	47	46.1	46.1		47.4	39.8	13.4	13.9	6	Tm 13.17
	7	59.1	59.1	60	59.1	59.1	51.7		37	11.6	11.1	7	B1
	8	61.7	61.7	62.6	60.7	61.7	60.2	63		10.2	8.3	8	AFP-3
	9	86.7	86.7	85.7	85.7	85.7	86.8	84.2	87.5		55.6	9	YL-1
	10	88.3	88.3	86.4	84.5	85.4	89.1	82.7	90.5	40.2		10	DAFP-1A
		1	2	3	4	5	6	7	8	9	10		

FIG 4.19

09376796-060701

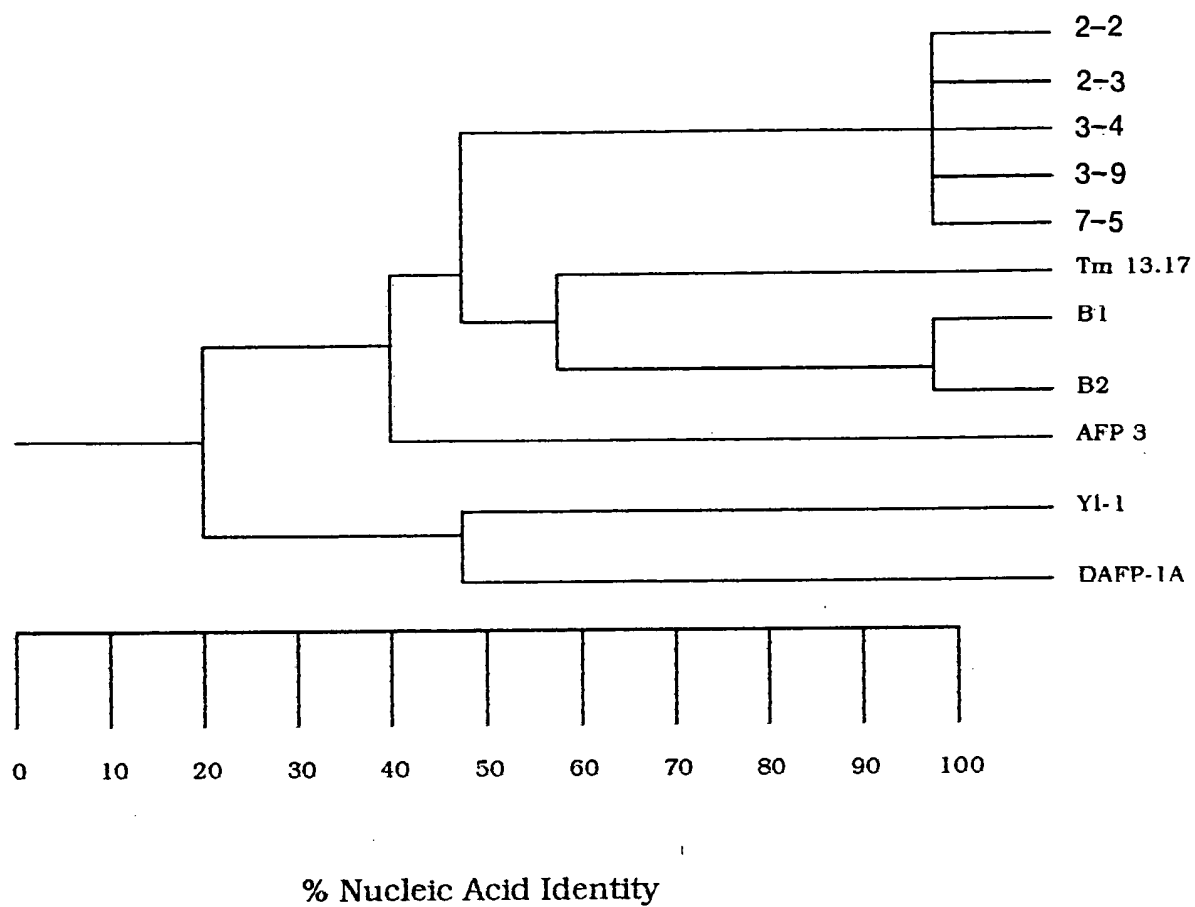


FIG 4.20

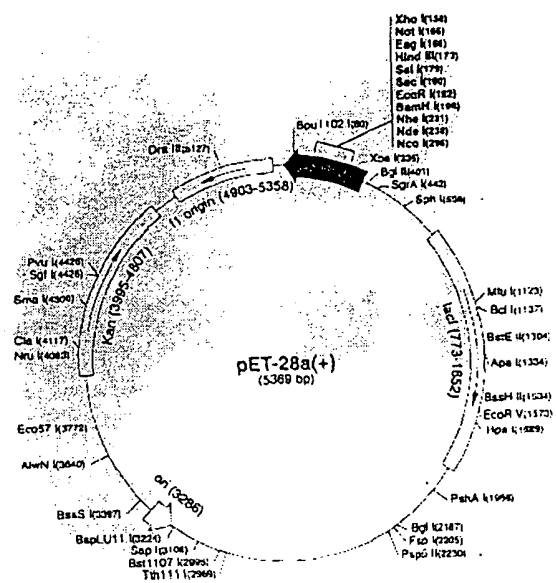
[illegible]

FIG. 5.0

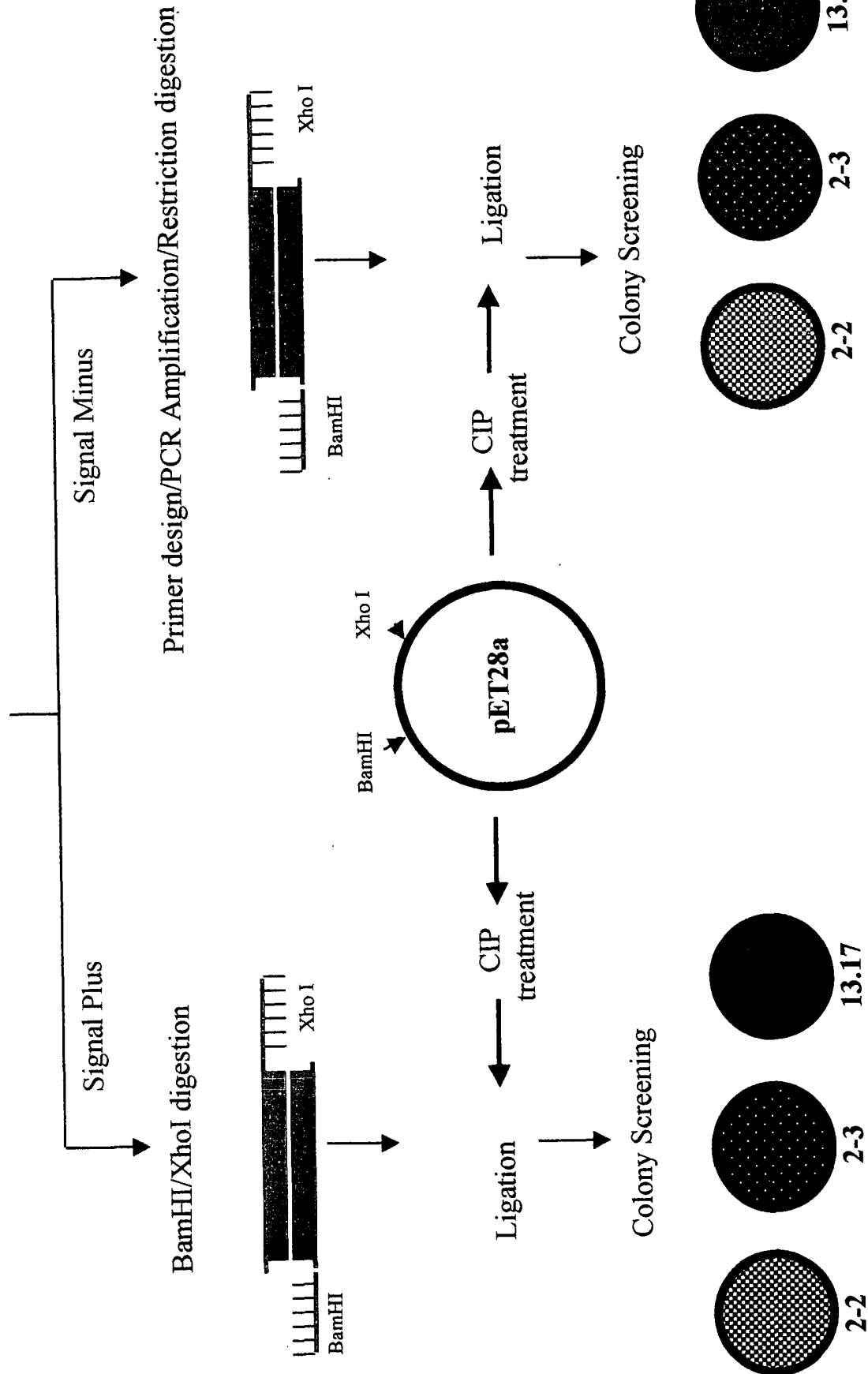
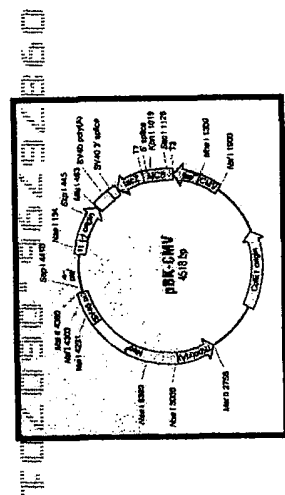


FIG. 5.1

09876796-060701

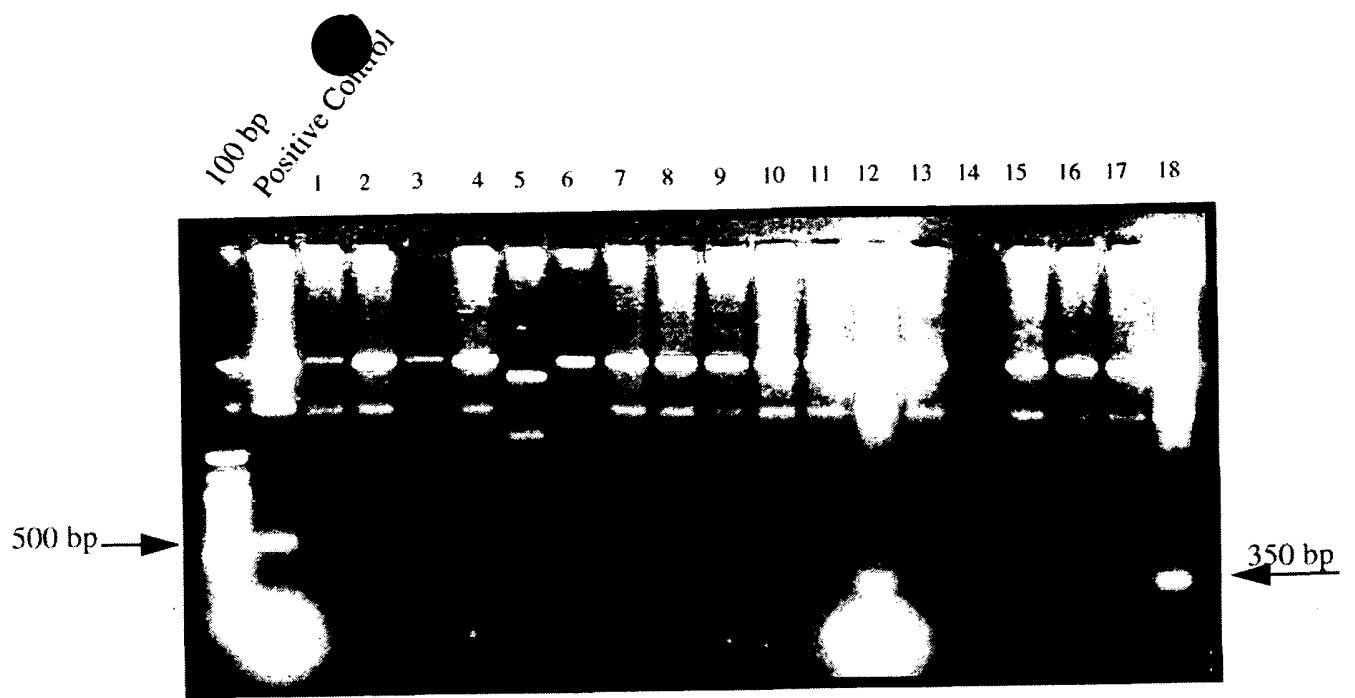


FIG. 5.2

0987560607080910111213141516

650 bp

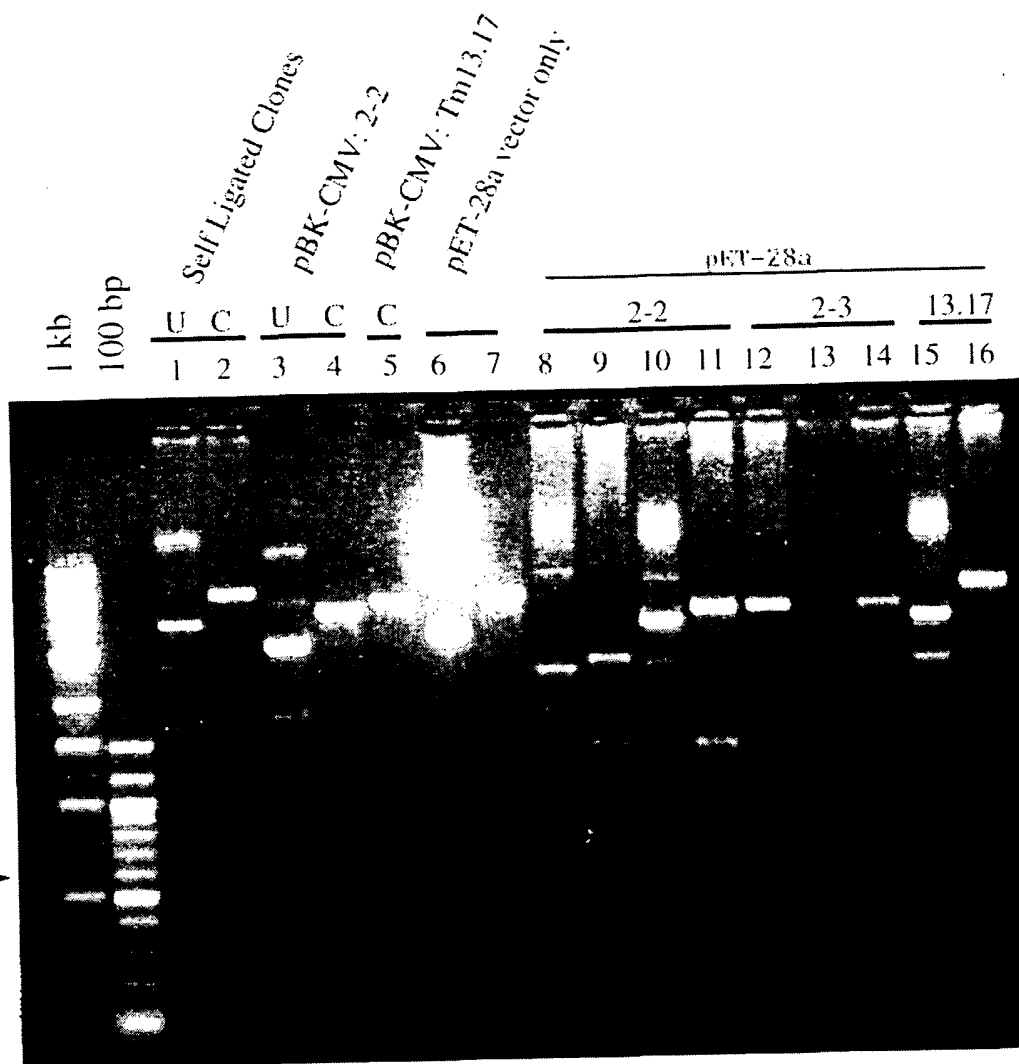


FIG. 5.3

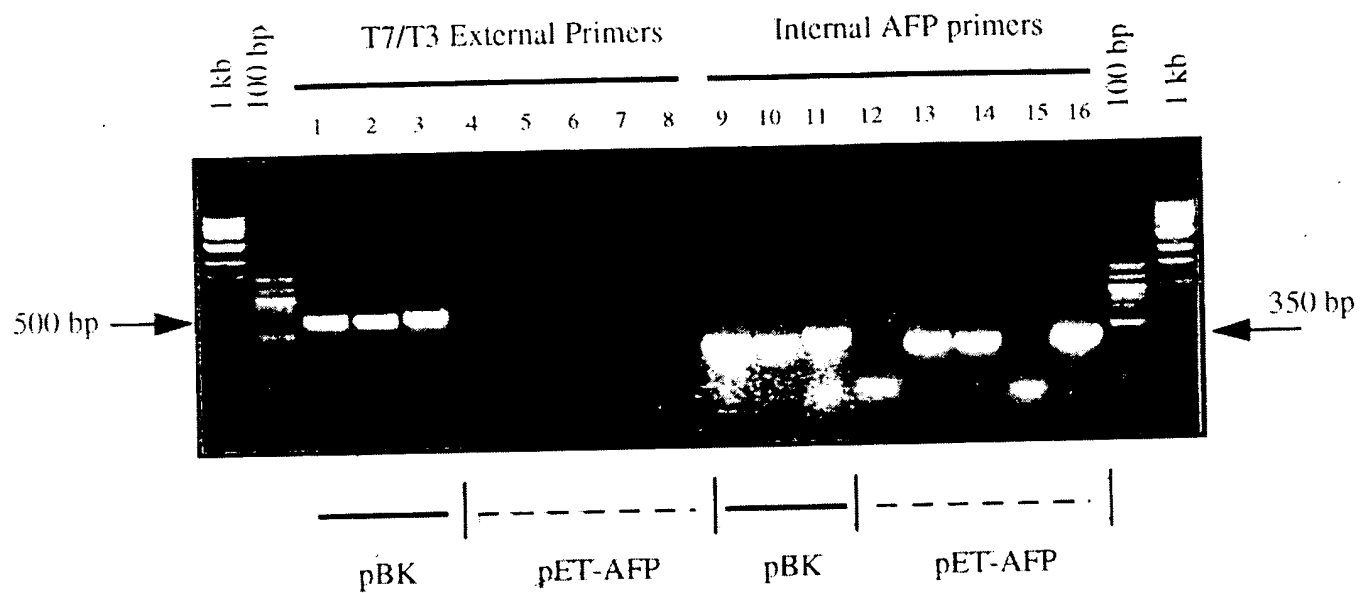


FIG. 5.4

09876543210

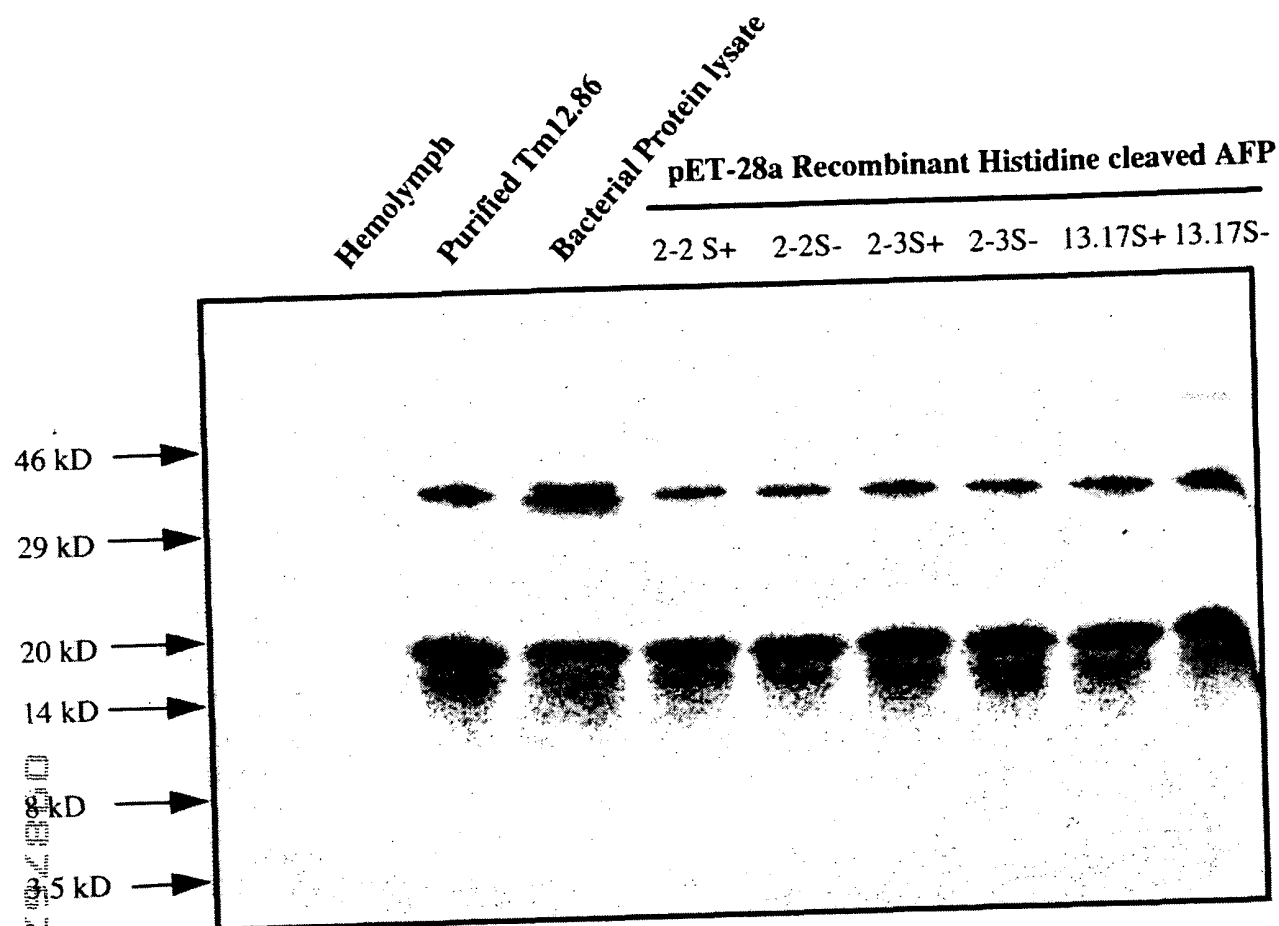


FIG. 5.6

His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTTAAG	50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96	
Met Gly Ser Ser His His His His His His Ser		
-55	-50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-45	-40	-35
AFP Start Codon		
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186	
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met		
-30	-25	-20
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT	231	
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala		
-15	-10	-5
N-terminal of mature AFP		
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276	
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser		
1	5	10
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321	
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp		
15	20	25
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366	
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys		
30	35	40
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411	
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala		
45	50	55
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456	
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val		
60	65	70
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501	
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val		
75	80	85
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546	
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys		
90	95	100
Stop Codon		
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGT	595	
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *		
105	110	115
Polyadenylation signal Poly-A tail		
TTTGA	CTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681	

FIG. 5.7

His-tagged clone 2.2 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA	CTTAAAG	50
His-tag Start Codon		
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96	
Met Gly Ser Ser His His His His His His Ser		
-30 -25		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141	
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-20 -15 -10		
N-terminal of mature AFP		
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186	
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln		
-5 1 5		
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231	
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val		
10 15 20		
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276	
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp		
25 30 35		
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321	
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr		
40 45 50		
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366	
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys		
55 60 65		
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411	
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile		
70 75 80		
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456	
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala		
85 90 95		
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501	
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser		
100 105 110		
Stop Codon		
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543	
Pro Ile Asp *		
115		

FIG. 5.8

His-tagged clone 2.3 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
AFP Start Codon	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
N-terminal of Mature AFP	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
Stop Codon	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
Polyadenylation signal Poly-A tail	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

FIG. 5.9

His-tagged Clone 2.3 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
<div>His-tag Start Codon</div> AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC <div>Met Gly Ser Ser His His His His His His Ser</div> <div>-30 -25</div>	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly <div>-20 -15 -10</div>	141
<div>N-terminal of mature AFP</div> GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln <div>-5 1 5</div>	186
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val <div>10 15 20</div>	231
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp <div>25 30 35</div>	276
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr <div>40 45 50</div>	321
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys <div>55 60 65</div>	366
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile <div>70 75 80</div>	411
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala <div>85 90 95</div>	456
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser <div>100 105 110</div>	501
<div>Stop Codon</div> CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT Pro Ile Asp * <div>115</div>	543

FIG. 5.10

His-tagged Tm 13.17 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-65 -60 -55	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-50 -45 -40	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile	
-35 -30 -25	
AFP Start Codon	
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC	231
Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser	
-20 -15 -10	
N-terminal of mature AFP	
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT	276
Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile	
-5 1 5	
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA	321
Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly	
10 15 20	
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG	366
Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu	
25 30 35	
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC	411
Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn	
40 45 50	
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG	456
Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu	
55 60 65	
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG	501
Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu	
70 75 80	
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG	546
Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu	
85 90 95	
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG	595
Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys	
100 105 110	
Stop Codon	
TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG	643
Phe Ser Pro Val Asp *	
115	
Polyadenylation signal Poly-A tail	
TGTGCTTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

FIG. 5.11

His-tagged Tm 13.17 without signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon	
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
N-terminal of mature AFP	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
Stop Codon	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

FIG. 5.12

FO/090" 96/9/860

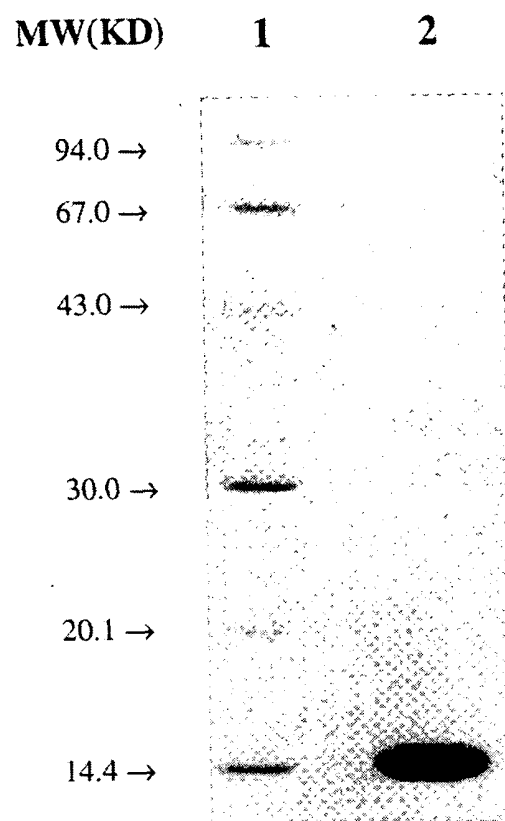


FIG. 6.0

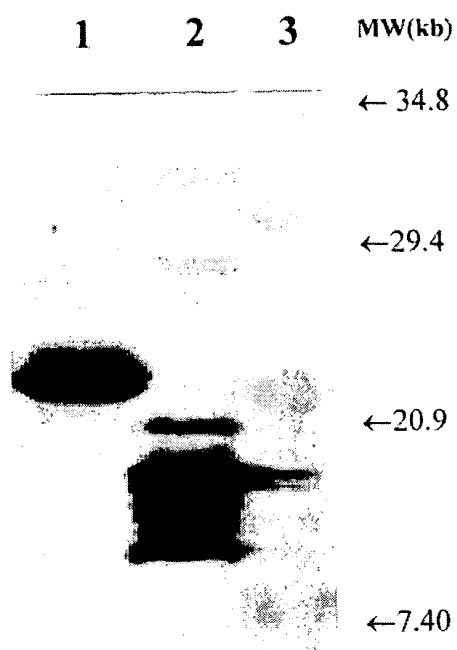


FIG. 6.1

09876798-060701



FIG. 6.2

FOI 90-95292860

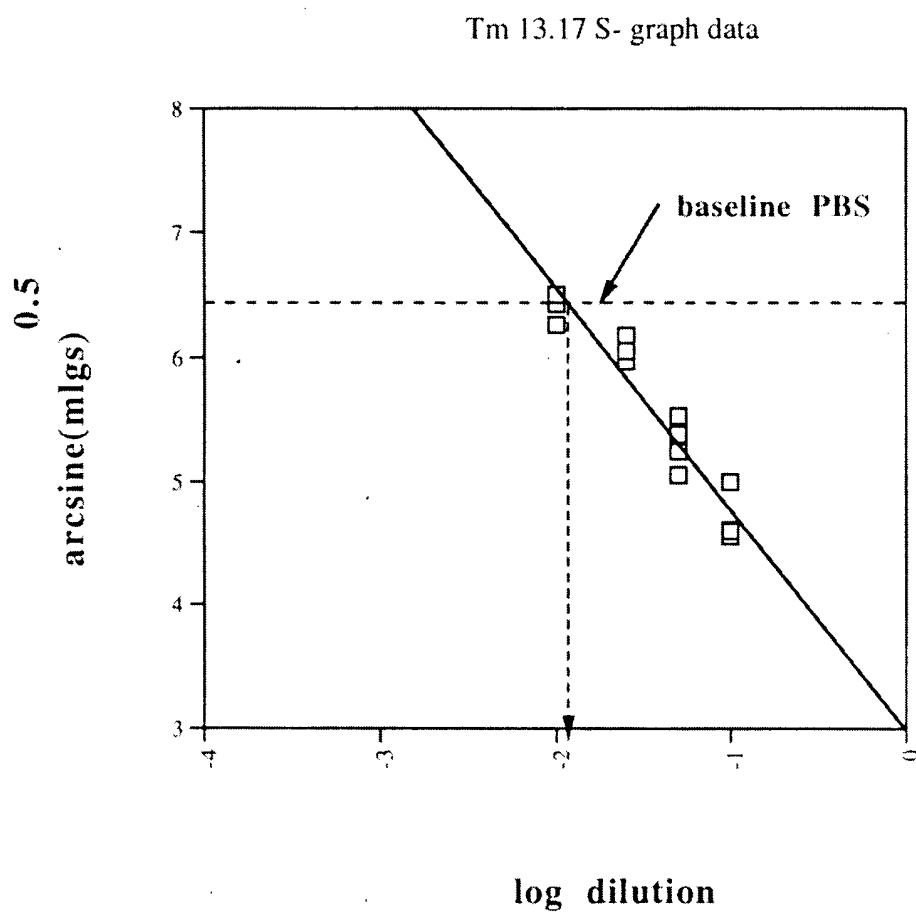


FIG. 6.3

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
A	Alanine	Ala	aliphatic	mod. hydrophobic	low
B	Asp or Asn	Asx			
C	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
H	Histidine	His	basic, imidazole	highly hydrophilic	high
I	Isoleucine	Ile	aliphatic	hydrophobic	low
J					
K	Lysine	Lys	basic	highly hydrophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
O					
P	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U					
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X					
Y	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Glx			
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

FIG. 7.1

09376796-060701

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of Tm 12.84	Tm13.17	Consensus with Tm 13.17	B1	Consensus with B1	AFP-3	Consensus with AFP-3
1	A	A	A	A	A	A	A	A		A	C	N
2	C	G	G	C	C	C	C	N		N	A	R
3	A	G	A	A	A	A	A	R		R	G	R
4	A	G	G	C	G	G	C	N		N	A	N
5	A	C	A	A	A	A	A	N		N	C	N
6	A	A	A	A	A	A	A	N		N	C	N
7	A	A	A	A	A	A	A	N		N	G	N
8	A	A	A	A	A	A	A	N		N	A	N
9	A	A	A	A	A	A	A	R		A	A	A
10	A	A	A	A	A	A	A	R		A	A	A
11	A	A	A	A	A	A	A	R		A	A	A
12	A	A	A	A	A	A	A	R		A	A	A
13	A	A	A	A	A	A	A	R	A?	A	A	A
14	T	G	T	G	T	G	G	G	T?	T	G	G
15	G	A	G	A	G	A	A	A	G?	G	A	A
16	A	A	A	A	A	A	A	A		A	A	A
17	A	A	A	A	A	A	A	R		R	A	A
18	A	C	C	C	C	C	T	Y		Y	G	Y
19	T	C	T	T	T	T	G	T		T	C	T
20	C	C	C	C	C	C	C	C	C/G	C	C	C
21	C	C	C	C	C	C	C	T		T	C	C
22	C	C	C	C	C	C	C	C		C	C	C
23	T	T	T	T	T	T	T	N		N	C	C
24	T	T	T	T	T	T	T	N		N	C	C
25	T	T	T	T	T	T	T	N		N	C	C
26	T	T	T	T	T	T	T	N		N	C	C
27	T	T	T	T	T	T	T	N		N	C	C
28	T	T	T	T	T	T	T	N		N	C	C
29	T	T	T	T	T	T	T	N		N	C	C
30	T	T	T	T	T	T	T	N		N	C	C
31	T	T	T	T	T	T	T	N		N	C	C
32	T	T	T	T	T	T	T	N		N	C	C
33	T	T	T	T	T	T	T	N		N	C	C
34	T	T	T	T	T	T	T	N		N	C	C
35	T	T	T	T	T	T	T	N		N	C	C
36	T	T	T	T	T	T	T	N		N	C	C
37	T	T	T	T	T	T	T	N		N	C	C
38	T	T	T	T	T	T	T	N		N	C	C
39	T	T	T	T	T	T	T	N		N	C	C
40	T	T	T	T	T	T	T	N		N	C	C
41	T	T	T	T	T	T	T	N		N	C	C
42	T	T	T	T	T	T	T	N		N	C	C
43	T	T	T	T	T	T	T	N		N	C	C
44	T	T	T	T	T	T	T	N		N	C	C
45	T	T	T	T	T	T	T	N		N	C	C
46	T	T	T	T	T	T	T	N		N	C	C
47	T	T	T	T	T	T	T	N		N	C	C
48	T	T	T	T	T	T	T	N		N	C	C
49	T	T	T	T	T	T	T	N		N	C	C
50	T	T	T	T	T	T	T	N		N	C	C
51	T	T	T	T	T	T	T	N		N	C	C
52	T	T	T	T	T	T	T	N		N	C	C
53	T	T	T	T	T	T	T	N		N	C	C
54	T	T	T	T	T	T	T	N		N	C	C
55	T	T	T	T	T	T	T	N		N	C	C
56	T	T	T	T	T	T	T	N		N	C	C
57	T	T	T	T	T	T	T	N		N	C	C
58	T	T	T	T	T	T	T	N		N	C	C
59	T	T	T	T	T	T	T	N		N	C	C
60	T	T	T	T	T	T	T	N		N	C	C
61	T	T	T	T	T	T	T	N		N	C	C
62	T	T	T	T	T	T	T	N		N	C	C
63	T	T	T	T	T	T	T	N		N	C	C
64	T	T	T	T	T	T	T	N		N	C	C
65	T	T	T	T	T	T	T	N		N	C	C
66	T	T	T	T	T	T	T	N		N	C	C
67	T	T	T	T	T	T	T	N		N	C	C
68	T	T	T	T	T	T	T	N		N	C	C
69	T	T	T	T	T	T	T	N		N	C	C
70	T	T	T	T	T	T	T	N		N	C	C
71	T	T	T	T	T	T	T	N		N	C	C
72	T	T	T	T	T	T	T	N		N	C	C
73	T	T	T	T	T	T	T	N		N	C	C
74	T	T	T	T	T	T	T	N		N	C	C
75	T	T	T	T	T	T	T	N		N	C	C
76	T	T	T	T	T	T	T	N		N	C	C
77	T	T	T	T	T	T	T	N		N	C	C
78	T	T	T	T	T	T	T	N		N	C	C
79	T	T	T	T	T	T	T	N		N	C	C
80	T	T	T	T	T	T	T	N		N	C	C
81	T	T	T	T	T	T	T	N		N	C	C
82	T	T	T	T	T	T	T	N		N	C	C
83	T	T	T	T	T	T	T	N		N	C	C
84	T	T	T	T	T	T	T	N		N	C	C
85	T	T	T	T	T	T	T	N		N	C	C
86	T	T	T	T	T	T	T	N		N	C	C
87	T	T	T	T	T	T	T	N		N	C	C
88	T	T	T	T	T	T	T	N		N	C	C
89	T	T	T	T	T	T	T	N		N	C	C
90	T	T	T	T	T	T	T	N		N	C	C
91	T	T	T	T	T	T	T	N		N	C	C
92	T	T	T	T	T	T	T	N		N	C	C
93	T	T	T	T	T	T	T	N		N	C	C
94	T	T	T	T	T	T	T	N		N	C	C
95	T	T	T	T	T	T	T	N		N	C	C
96	T	T	T	T	T	T	T	N		N	C	C
97	T	T	T	T	T	T	T	N		N	C	C
98	T	T	T	T	T	T	T	N		N	C	C
99	T	T	T	T	T	T	T	N		N	C	C
100	T	T	T	T	T	T	T	N		N	C	C
101	T	T	T	T	T	T	T	N		N	C	C
102	T	T	T	T	T	T	T	N		N	C	C
103	T	T	T	T	T	T	T	N		N	C	C
104	T	T	T	T	T	T	T	N		N	C	C
105	T	T	T	T	T	T	T	N		N	C	C
106	T	T	T	T	T	T	T	N		N	C	C
107	T	T	T	T	T	T	T	N		N	C	C
108	T	T	T	T	T	T	T	N		N	C	C
109	T	T	T	T	T	T	T	N		N	C	C
110	T	T	T	T	T	T	T	N		N	C	C
111	T	T	T	T	T	T	T	N		N	C	C
112	T	T	T	T	T	T	T	N		N	C	C
113	T	T	T	T	T	T	T	N		N	C	C
114	T	T	T	T	T	T	T	N		N	C	C
115	T	T	T	T	T	T	T	N		N	C	C
116	T	T	T	T	T	T	T	N		N	C	C
117	T	T	T	T	T	T	T	N		N	C	C

FIG. 7.2

09876796 "060701
T 0 2 0 9 0 " 9 6 7 9 6

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
118	C	C	C	C	C	C	A	N	A	N	G	N
119	A	A	A	A	A	A	A	A	C	N	C	N
120	G	G	G	G	G	G	T	N	T	G	T	N
121	G	G	G	G	G	G	A	G	A	A	G	G
122	T	T	T	T	T	T/A	A	T/A	A	T/A	A	A/T
123	G	T	T	T	T	G	A	R	A	T/A	A	R
124	T	T	T	T	T	T	A	T/A	A	C/G	T	T/G
125	C	C	C	C	C	C	G	Y	G	Y	T	C/G
126	C	G	G	G	G	G	T	G	G	G	G	G
127	G	G	G	G	G	G	G	G	A	A	A	A
128	A	A	A	A	A	A	A	A	G	A	G	G
129	A	A	A	A	A	A	T	T	T	T	T	T
130	G	T	T	T	T	T	G	G	G	G	G	G
131	T	T	T	T	T	T	T	T	T	T	T	T
132	G	T	T	T	T	T	G	T	T	T	T	T
133	T	T	T	T	T	T	T	T	T	T	T	T
134	C	C	C	C	C	C	C	C	C	C	C	C
135	C	C	C	C	C	C	C	C	C	C	C	C
136	C	C	C	C	C	C	C	C	C	C	C	C
137	A	A	A	A	A	A	A	A	A	A	A	A
138	A	A	A	A	A	A	A	A	A	A	A	A
139	A	A	A	A	A	A	A	A	A	A	A	A
140	A	A	A	A	A	A	A	A	A	A	A	A
141	A	A	A	A	A	A	A	A	A	A	A	A
142	A	A	A	A	A	A	A	A	A	A	A	A
143	C	C	C	C	C	C	A	A	C	G/C	T	G/C
144	G	G	G	G	G	G	T	Y	G	R	C	N
145	A	A	A	A	A	A	C	G/C	A	G/C	C	G/C
146	T	T	T	T	T	T	A	T	A	A	C	N
147	C	C	C	C	C	C	A	N	A	N	C	N
148	G	G	G	G	G	G	A	R	A	R	A	R
149	A	A	A	A	A	A	C	N	A	C/G	A	C/G
150	C	C	C	C	C	C	C	C	A	A	A	A
151	A	A	A	A	A	A	A	A	A	A	A	A
152	A	A	A	A	A	A	A	A	A	A	A	A
153	A	A	A	A	A	A	A	A	A	A	A	A
154	G	G	G	G	G	G	G	G	A	G	G	G
155	T	T	T	T	T	T	C	Y	C	Y	T	T
156	C	C	C	C	C	C	C	C	C	C	C	C
157	C	C	C	C	C	C	C	C	C	C	C	C
158	G	G	G	G	G	G	C	G	C	A	A	A
159	C	C	C	C	C	C	C	C	A	N	A	A
160	A	A	A	A	A	A	A	A	A	N	A	A
161	C	C	C	C	C	C	A	N	A	N	C	N
162	A	A	A	A	A	A	C	N	A	N	C	N
163	G	G	G	G	G	G	G	G	G	G	G	G
164	G	G	G	G	G	G	G	G	G	G	G	G
165	T	T	T	T	T	T	T	T	T	T	T	T
166	G	G	G	G	G	G	G	G	G	G	G	G
167	T	T	T	T	T	T	A	T/A	A	T/A	A	T/A
168	C	C	C	C	C	C	C	C	C	C	C	C
169	T	T	T	T	T	T	T	N	T	N	A	N
170	T	T	T	T	T	T	T	G	G	G	A	A
171	G	G	G	G	G	G	G	G	G	G	A	A
172	T	T	T	T	T	T	A	T/A	A	T/A	T	T/A
173	C	C	C	C	C	C	G	C/G	G	C/G	G	C/G
174	G	G	G	G	G	G	G	G	G	G	G	G
175	A	A	A	A	A	A	A	A	A	A	A	A
176	T	T	T	T	T	T	C	Y	C	Y	A	A
177	A	A	A	A	A	A	G	A	A	A	A	A
178	G	G	G	G	G	G	A	G	A	G	A	A
179	A	A	A	A	A	A	T	T	T	T	A	A
180	C	C	C	C	C	C	C	C	C	C	C	C
181	C	C	C	C	C	C	C	C	C	C	C	C
182	C	C	C	C	C	C	C	C	C	C	C	C
183	C	C	C	C	C	C	C	C	C	C	C	C
184	A	A	A	A	A	A	A	A	A	A	A	A
185	A	A	A	A	A	A	A	A	A	A	A	A
186	A	A	A	A	A	A	A	A	A	A	A	A
187	A	A	A	A	A	A	A	A	A	A	A	A
188	T	T	T	T	T	T	T	N	T	N	T	T
189	G	G	G	G	G	G	A	O	G	A	G	A
190	A	A	A	A	A	A	A	A	A	A	A	A
191	A	A	A	A	A	A	A	A	A	A	A	A
192	G	G	G	G	G	G	A	R	A	R	A	A
193	A	A	A	A	A	A	A	N	A	N	A	A
194	A	A	A	A	A	A	C	R	A	R	A	A
195	G	G	G	G	G	G	G	R	A	R	A	A
196	C	C	C	C	C	C	C	G/C	C	G/C	C	C
197	A	A	A	A	A	A	A	A	A	A	A	A
198	C	C	C	C	C	C	A	N	A	N	A	A
199	G	G	G	G	G	G	G	G	C	G	G	G
200	T	T	T	T	T	T	T	T	T	T	T	T
201	C	C	C	C	C	C	T	Y	T	Y	T	Y
202	C	C	C	C	C	C	T	Y	T	Y	T	Y
203	T	T	T	T	T	T	T	T	T	T	T	T
204	C	C	C	C	C	C	T	T	T	T	T	T
205	T	T	T	T	T	T	T	T	T	T	T	T
206	C	C	C	C	C	C	G	C	C	C	C	C
207	T	T	T	T	T	T	T	N	A	N	A	A
208	T	T	T	T	T	T	T	T	T	T	T	T
209	T	T	T	T	T	T	T	T	T	T	T	T
210	C	C	C	C	C	C	G	C/G	T	N	C	N
211	T	T	T	T	T	T	C	N	T	N	T	N
212	C	C	C	C	C	C	C	G/C	T	Y	G	G/C
213	A	A	A	A	A	A	A	A	A	A	A	A
214	A	A	A	A	A	A	A	A	A	A	A	A
215	A	A	A	A	A	A	A	A	A	A	A	A
216	A	A	A	A	A	A	A	A	A	A	A	A
217	A	A	A	A	A	A	A	A	A	A	A	A
218	A	A	A	A	A	A	A	A	A	A	A	A
219	A	A	A	A	A	A	A	A	A	A	A	A
220	A	A	A	A	A	A	A	A	A	A	A	A
221	T	T	T	T	T	T	C	Y	C	Y	C	C
222	G	G	G	G	G	G	G	G	A	R	A	A
223	A	A	A	A	A	A	A	A	A	A	A	A
224	G	G	G	G	G	G	A	A/T	A	A/T	A	A/T
225	A	A	A	A	A	A	T	G/C	T	N	T	N
226	G	G	G	G	G	G	G	G	A	R	C	R
227	T	T	T	T	T	T	G	T	A	T	T	T
228	G	G	G	G	G	G	G	G	A	T	T	T
229	C	C	C	C	C	C	C	C	A	C	A	A
230	A	A	A	A	A	A	A	A	C	N	C	N
231	A	A	A	A	A	A	A	A	C	C	C	C
232	A	A	A	A	A	A	A	A	C	C	C	C
233	C	C	C	C	C	C	C	C	C	C	C	C
234	C	C	C	C	C	C	C	C	C	C	C	C
235	G	G	G	G	G	G	G	G	G	G	G	G

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
236	A	A	A	A	A	A	A	A	A	A	A	N
237	A	G	A	A	A	A	A	A	A	A	C	N
238	G	C	G	G	G	G	T	N	T	N	A	N
239	C	C	C	C	C	C	C	C	C	C	G	C/G
240	C	C	C	C	C	C	G	G	G	G	T	N
241	G	G	G	G	G	G	G	G	G	G	G	G
242	G	G	G	G	G	G	A	A	A	A	T	A/T
243	A	A	A	A	A	A	A	A	A	A	G	G
244	A	A	A	A	A	A	A	A	A	A	A	A
245	A	C	A	A	A	A	A	A	A	A	N	N
246	A	C	A	A	A	A	A	C/G	A	A	T	N
247	A	C	A	A	A	A	A	R	A	R	T	Y
248	C	C	C	C	C	C	T	Y	T	Y	T	N
249	C	C	C	C	C	C	G	C/G	T	N	C	N
250	A	A	A	A	A	A	G	R	G	R	C	N
251	A	A	A	A	A	A	T	A/T	A	A/T	A	A/T
252	T	T	T	T	T	T	G	N	G	N	C	N
253	T	T	T	T	T	T	T	G	G	G	T	G/C
254	G	G	G	G	G	G	C	G/C	C	G/C	G	Y
255	G	G	G	G	G	G	G	G	G	G	G	G
256	A	A	A	A	A	A	A	A	A	A	A	A
257	G	G	G	G	G	G	A	G/C	C	G/C	C	G/C
258	G	G	G	G	G	G	G	G	A	R	C	N
259	G	T	T	T	T	T	T	T	C	Y	A	N
260	T	A	A	A	A	A	T	R	G	R	C	N
261	A	C	C	C	C	C	T	Y	C	Y	A	N
262	C	T	T	T	T	T	T	T	T	Y	T	N
263	C	C	C	C	C	C	G	C/G	C	C/G	T	N
264	A	A	A	A	A	A	A	A	A	A	A	A
265	A	A	A	A	A	A	G	A	A	R	A	R
266	A	A	A	A	A	A	G	R	G	R	G	R
267	G	G	G	G	G	G	G	N	A	G	A	N
268	C	C	C	C	C	C	A	C/G	G	C/G	C	C/G
269	C	C	C	C	C	C	G	A	A	A	A	A
270	A	A	A	A	A	A	A	A	A	A	A	A
271	A	A	A	A	A	A	A	A	A	A	A	A
272	G	G	G	G	G	G	G	A	A	A	A	A
273	C	C	C	C	C	C	T	C/G	T	N	T	N
274	T	T	T	T	T	T	T	T	T	T	T	T
275	G	A	A	A	A	A	G	G	G	G	C	G/C
276	A	A	A	A	A	A	A	A	A	A	A	A
277	A	A	A	A	A	A	G	R	C	N	A	N
278	G	G	G	G	G	G	G	G	A	G	G	N
279	C	C	C	C	C	C	C	N	A	N	G	N
280	A	A	A	A	A	A	A	A	G	R	A	N
281	T	T	T	T	T	T	G	N	T	N	A	N
282	G	G	G	G	G	G	T	G	A	N	A	N
283	T	T	T	T	T	T	C	G/C	C	N	C	N
284	G	G	G	G	G	G	A	R	A	N	T	N
285	C	C	C	C	C	C	C	C	A	N	C	N
286	C	C	C	C	C	C	A	Y	A	N	C	N
287	C	C	C	C	C	C	T	R	A	N	T	N
288	A	A	A	A	A	A	G	R	A	N	G	N
289	G	G	G	G	G	G	A	R	C	N	G	N
290	C	C	C	C	C	C	C	C	A	C/G	A	C/G
291	C	C	C	C	C	C	A	A	A	A	G	R
292							A	C	T	A	A	A/T
293							C	G	G	C/G	T	N
294							A	C	A	R	C	N
295	G	G	G	G	G	G	A	C	A	A/T	T	N
296	A	A	A	A	A	A	A	C	A	R	C	C/G
297	C	C	C	C	C	C	A	G	A	A/T	G	R
298	G	A	A	A	A	A	A	G	A	C/G	A	A
299	A	A	A	A	A	A	A	A	A	R	A	R
300	A	A	A	A	A	A	A	A	A	A	A	A
301	G	A	A	A	A	A	A	R	A	R	A	A
302	G	T	T	T	T	T	T	Y	C	Y	G	R
303	T	G	G	G	G	G	G	N	G	N	T	N
304	G	A	A	A	A	A	A	O	A	R	A	R
305	A	C	C	C	C	C	A	C/G	A	R	A	R
306	A	A	A	A	A	A	A	A	A	A	A	A
307	A	A	A	A	A	A	A	A	A	A	A	A
308	A	A	A	A	A	A	A	A	A	A	A	A
309	A	A	A	A	A	A	A	A	A	A	A	A
310	A	A	A	A	A	A	A	A	A	A	A	A
311	A	A	A	A	A	A	A	A	A	A	A	A
312	A	A	A	A	A	A	A	A	A	A	A	A
313	A	A	A	A	A	A	A	A	A	A	A	A
314	T	T	T	T	T	T	C	T	T	A/T	T	A/T
315	C	C	C	C	C	C	C	C	G	C/G	T	C/G
316	G	G	G	G	G	G	A	T	T	N	G	Y
317	T	T	T	T	T	T	C	T	C	Y	T	N
318	G	C	C	C	C	C	A	G/C	G	G/C	T	N
319	C	A	A	A	A	A	A	N	A	N	G	N
320	A	G	A	A	A	A	A	A	A	N	C	N
321	G	A	A	A	A	A	T	N	A	A	A	A
322	A	A	A	A	A	A	A	A	A	R	A	R
323	G	A	A	A	A	A	G	G	T	N	A	N
324	T	T	T	T	T	T	T	T	G	N	T	N
325	G	G	G	G	G	G	G	G	C	G/C	G	G/C
326	C	C	C	C	C	C	C	C	A	N	T	N
327	G	T	T	T	T	T	G	Y	C	G/C	C	G/C
328	T	G	G	G	G	G	G	G	G	N	C	N
329	G	T	T	T	T	T	C	G	T	G/C	C	N
330	G	T	T	T	T	T	T	G	T	N	C	N
331	T	T	T	T	T	T	T	T	A	N	T	N
332	C	C	C	C	C	C	C	C	A	N	C	N
333	A	A	A	A	A	A	A	A	T	N	A	N
334	A	A	A	A	A	A	A	A	G	N	A	N
335	G	A	A	A	A	A	A	A	A	A	A	A
336	A	A	A	A	A	A	A	A	A	A	A	A
337	A	A	A	A	A	A	A	A	A	A	A	A
338	A	A	A	A	A	A	A	A	A	A	A	A
339	G	G	G	G	G	G	A	R	C	R	A	R
340	G	G	G	G	G	G	G	N	A	N	G	N
341	C	C	C	C	C	C	T	Y	A	N	A	N
342	C	C	C	C	C	C	A	A	C	N	C	N
343	A	A	A	A	A	A	C	C	T	Y	T	Y
344	C	C	C	C	C	C	T	A/T	C	N	C	N
345	A	A	A	A	A	A	G	C/G	G	C/G	C	C/G
346	C	C	C	C	C	C	T	Y	A	N	C	N
347	A	A	A	A	A	A	T	A/T	G	R	T	N
348	G	G	G	G	G	G	A	R	A	A	A	A
349	A	A	A	A	A	A	A	G	A	R	C	N
350	G	G	G	G	G	G	A	A	A	A	A	A
351	G	G	G	G	G	G	A	R	A	R	A	N
352	A	A	A	A	A	A	A	A	A	A	A	A
353	A	A	A	A	A	A	A	A	A	A	A	A/T

FIG. 7.2 Cont.

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Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
354	A	A	A	A	A	A	G	R	A	R	C	N
355	A	A	A	A	A	A	A	A	C	N	T	N
356	C	C	C	C	C	C	C	C	G	C/G	C	C/G
357	G	G	G	G	G	G	G	G	G	G/C	T	G/C
358	C	C	C	C	C	C	T	Y	A	N	C	N
359	T	T	T	T	T	T	T	N	T	N	A	N
360	T	T	T	T	T	T	T	T	T	T	G	N
361	A	A	A	A	A	A	T	A/T	T	A/T	C	N
362	T	T	T	T	T	T	T	Y	G	N	A	N
363	A	A	A	A	A	A	C	R	A	R	C	N
364	G	G	G	G	G	G	A	A	A	N	G	R
365	A	A	A	A	A	A	A	Y	A	N	A	A
366	C	C	C	C	C	C	T	A	T	A/T	C	A/T
367	A	A	A	A	A	A	C	Y	T	Y	T	Y
368	C	C	C	C	C	C	T	T	A	N	T	N
369	T	T	T	T	T	T	T	T	C	Y	T	Y
370	T	T	T	T	T	T	C	T	A	Y	T	N
371	C	C	C	C	C	C	A	A	A	N	A	A
372	A	A	A	A	A	A	A	A	A	A	A	A
373	A	A	A	A	A	A	A	R	A	N	A	N
374	G	G	G	G	G	G	T	N	T	N	T	N
375	T	T	T	T	T	T	G	N	G	N	C	N
376	G	G	G	G	G	G	T	T	T	N	G	N
377	T	T	T	T	T	T	A	R	G	N	C	N
378	A	A	A	A	A	A	T	T	A	N	T	N
379	T	T	T	T	T	T	C	Y	T	N	T	N
380	T	T	T	T	T	T	A	T	T	T/A	T	T/A
381	T	T	T	T	T	T	T	Y	T	Y	C	Y
382	A	A	A	A	A	A	A	T/A	T	T/A	A	N
383	C	C	C	C	C	C	G	C/G	A	N	A	N
384	G	G	G	G	G	G	A	R	A	R	G	R
385	A	A	A	A	A	A	A	A	G	N	A	A
386	C	C	C	C	C	C	A	N	A	N	T	N
387	A	A	A	A	A	A	A	A	G	N	A	A
388	C	C	C	C	C	C	A	R	A	N	A	N
389	G	G	G	G	G	G	A	Y	C	N	C	N
390	A	A	A	A	A	A	A	A	A	A	G	A
391	A	A	A	A	A	A	G	R	C	N	G	Y
392	A	A	A	A	A	A	C	C	C	C	T	C
393	C	C	C	C	C	C	A	T/A	A	T/A	G	N
394												
395												
396												
397	G	G	G	G	G	G	A	R	A	R		
398	T	T	T	T	T	T	T	A	T	A/T		
399	T	T	T	T	T	T	T	N	T	N		
400	T	T	T	T	T	T	T	T	T	T		
401	T	T	T	T	T	T	T	T	T	T		
402	C	C	C	C	C	C	C	C	T	Y		
403	T	T	T	T	T	T	T	T	T	T		
404	C	C	C	C	C	C	C	T	T	Y		
405	T	T	T	T	T	T	C	C	G	N		
406	C	C	C	C	C	C	A	C	A	C		
407	C	C	C	C	C	C	C	C	A	N		
408	T	T	T	T	T	T	T	T	T	N		
409	T	T	T	T	T	T	T	T	T	N		
410	A	A	A	A	A	A	T	T	A	R		
411	T	T	T	T	T	T	T	T	T	T		
412	G	G	G	G	G	G	T	A	T	Y		
413	A	A	A	A	A	A	A	T	T	T		
414	T	T	T	T	T	T	T	T	T	A/T		
415	T	T	T	T	T	T	T	T	T	T		
416	T	T	T	T	T	T	T	T	T	T		
417	T	T	T	T	T	T	T	T	T	T		
418	A	A	A	A	A	A	T	A	T	T		
419	A	A	A	A	A	A	T	T	T	T		
420	T	T	T	T	T	T	T	T	T	T		
421	T	T	T	T	T	T	T	T	T	T		
422	G	G	G	G	G	G	T	G	C	Y		
423	T	T	T	T	T	T	T	T	A	N		
424	T	T	T	T	T	T	T	T	A	N		
425	T	T	T	T	T	T	T	T	A	N		
426	T	T	T	T	T	T	T	T	A	N		
427	G	G	G	G	G	G	T	G	C	N		
428	T	T	T	T	T	T	A	T	T	T		
429	A	A	A	A	A	A	T	T	T	T		
430	T	T	T	T	T	T	T	T	T	T		
431	T	T	T	T	T	T	T	T	T	T		
432	G	G	G	G	G	G	T	T	T	T		
433	A	A	A	A	A	A	G	T	T	T		
434	C	C	C	C	C	C	R	N	T	T		
435	T	T	T	T	T	T	C	T	T	T		
436	G	G	G	G	G	G	A	T	T	T		
437	A	A	A	A	A	A	T	G	T	T		
438	A	A	A	A	A	A	T	A	T	T		
439	A	A	A	A	A	A	T	G	T	T		
440	T	T	T	T	T	T	T	T	T	T		
441	T	T	T	T	T	T	T	T	T	T		
442	T	T	T	T	T	T	T	T	T	T		
443	T	T	T	T	T	T	T	T	T	T		
444	G	G	G	G	G	G	A	A	A	A		
445	A	A	A	A	A	A	A	A	A	A		
446	C	C	C	C	C	C	T	N	T	T		
447												
448												
449												
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471												

FIG. 7.2 Cont.

Position	Tm 12.84-2.2	Tm 12.84-2.3	Tm 12.84-3.4	Tm 12.84-3.9	Tm 12.84-7.5	Consensus of	Tm13.17	Consensus with	B1	Consensus with	AFP-3	Consensus with
472	A	A	A	A	A	A	A	A	A	A	A	A
473	A	A	A	A	A	A	A	A	A	A	A	A
474	T	T	T	T	T	T	T	T	T	T	T	T
475	A	A	A	A	A	A	A	A	A	A	A	A
476	A	A	A	A	A	A	A	A	A	A	A	A
477	A	A	A	A	A	A	A	A	A	A	A	A
478	G	G	G	G	G	G	G	G	G	G	T	N
479	G	G	G	G	G	G	T	N	N	N	T	N
480	T	T	T	T	T	T	G	N	N	N	T	N
481	A	A	A	A	A	A	T	N	N	N	A	N
482	A	C	C	C	C	C	T	Y	Y	Y	A	N
483	T	T	T	T	T	T	T	T	T	T	A	AT
484	A	A	A	A	A	A	C	N	N	N	G	N
485	T	T	T	T	T	T	T	T	T	T	A	AT
486	C	C	C	C	C	C	G	N	N	N	A	N
487	G	G	G	G	G	G	A	R	R	R	A	R
488	T	T	T	T	T	T	T	T	T	T	A	T/A
489	T	T	T	T	T	T	G	N	N	N	A	N
490	A	A	A	A	A	A	A	N	N	N	A	N
491	T	T	T	T	T	T	A	R	R	R	A	R
492	G	G	G	G	G	G	A	N	N	N	A	N
493	T	A	T	A	A	A	A	A	A	A	A	A
494	A	A	A	A	A	A	A	A	A	A	A	A
495	A	A	A	A	A	A	A	A	A	A	A	A
496	A	A	A	A	A	A	A	A	A	A	A	A
497	A	A	A	A	A	A	A	A	A	A	A	A
498	A	A	A	A	A	A	A	A	A	A	A	A
499	A	A	A	A	A	A	A	A	A	A	A	A
500	A	A	A	A	A	A	A	A	A	A	A	A
501	A	A	A	A	A	A	A	A	A	A	A	A
502	A	A	A	A	A	A	A	A	A	A	A	A
503	A	A	A	A	A	A	A	A	A	A	A	A
504	A	A	A	A	A	A	A	A	A	A	A	A
505	A	A	A	A	A	A	A	A	A	A	A	A
506	A	A	A	A	A	A	A	A	A	A	A	A
507	A	A	A	A	A	A	A	A	A	A	A	A
508	A	A	A	A	A	A	A	A	A	A	A	A
509	A	A	A	A	A	A	A	A	A	A	A	A
510	A	A	A	A	A	A	A	A	A	A	A	A
511	A	A	A	A	A	A	A	A	A	A	A	A
512	A	A	A	A	A	A	A	A	A	A	A	A

FIG. 7.2 Cont.

092679-060701

Position	Tm 1264.22	Tm 1264.23	Tm 1264.34	Tm 1264.39	Tm 1264.75	Consensus	Tm 12.17	Consensus	Tm P-01	Tm P-02	Consensus	Tm AFP-3	Consensus	GENERAL	SUBSTITUTIONS - mod to lead common
98	V	D	V	V	V	V	T	ALP/ALH	S	S	ALP/ALH	V	ALP/ALH	V	S
99	K	K	K	K	K	K	E	ACD	E	E	ACD	D	ACD	D	E
100	K	K	K	K	K	K	K	K	K	K	K	D	K	K	L
101	V	V	V	V	V	V	V	ALP	V	V	ALP	V	ALP	V	L
102	V	V	V	V	V	V	V	ALP	V	V	ALP	V	ALP	V	I
103	Q	Q	Q	Q	Q	Q	K	ACD	E	E	ACD	A	ACD	Q	E
104	K	K	K	K	K	K	K	K	K	K	K	A	K	K	N
105	C	C	C	C	C	C	V	ALP	V	V	ALP	C	ALP	C	A
106	V	V	V	V	V	V	V	ALP/ALH	V	V	ALP/ALH	A	ALP/ALH	V	T
107	V	V	V	V	V	V	V	HY*, ACDBAS	V	V	HY*, ACDBAS	V	HY*, ACDBAS	V	A
108	K	K	K	K	K	K	K	HY*, ACDBAS	V	V	HY*, ACDBAS	V	HY*, ACDBAS	V	E
109	K	K	K	K	K	K	K	HY*, ACDBAS	V	V	HY*, ACDBAS	V	HY*, ACDBAS	V	E
110	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
111	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
112	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
113	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
114	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
115	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
116	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
117	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
118	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
119	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
120	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
121	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
122	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
123	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
124	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
125	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
126	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
127	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
128	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
129	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
130	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
131	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
132	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
133	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
134	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
135	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
136	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A
137	T	T	T	T	T	T	T	ALP	T	T	ALP	T	ALP	T	A

FIG. 7.3 Cont.

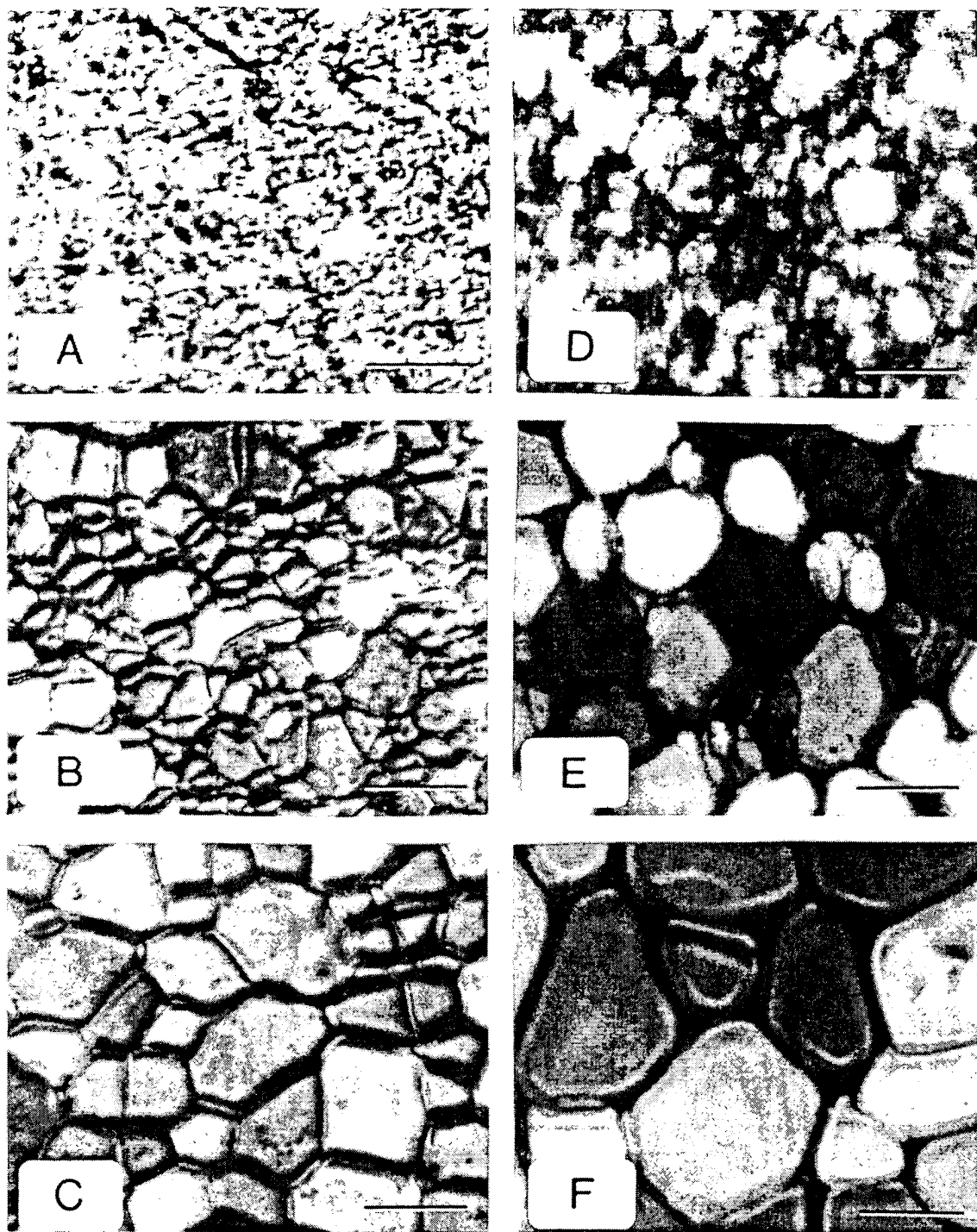


FIG. 8.0

09876796-060701

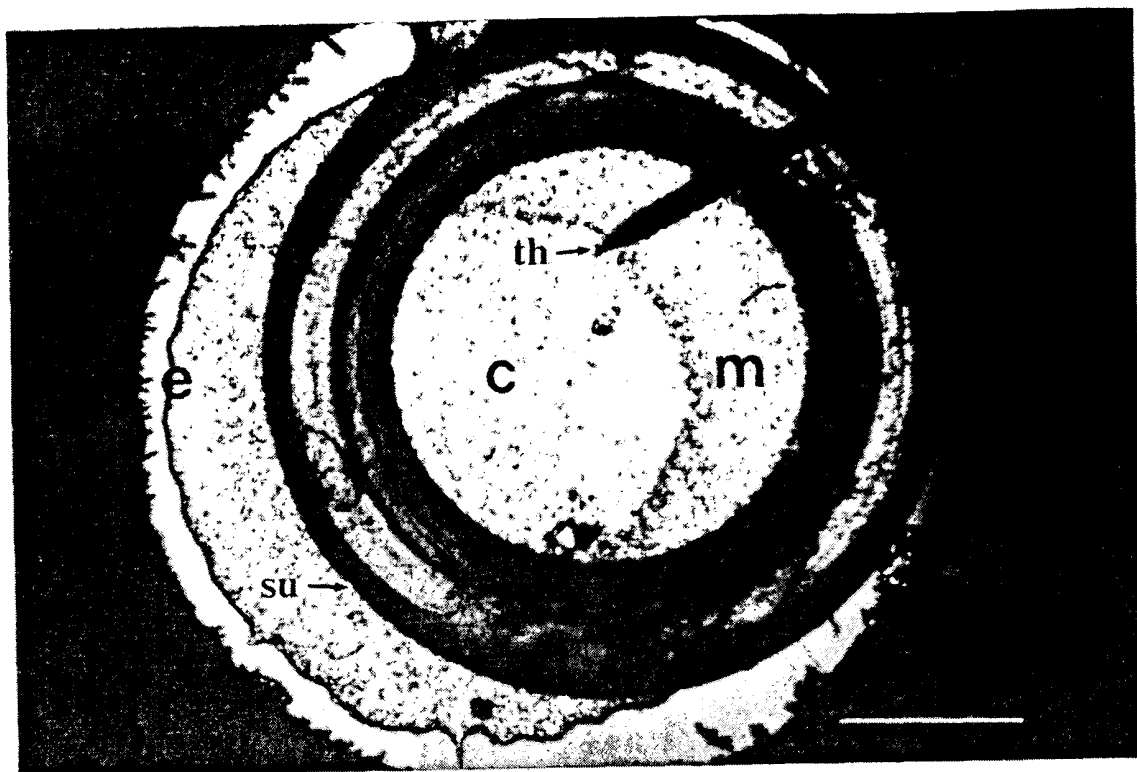


FIG. 8.1a

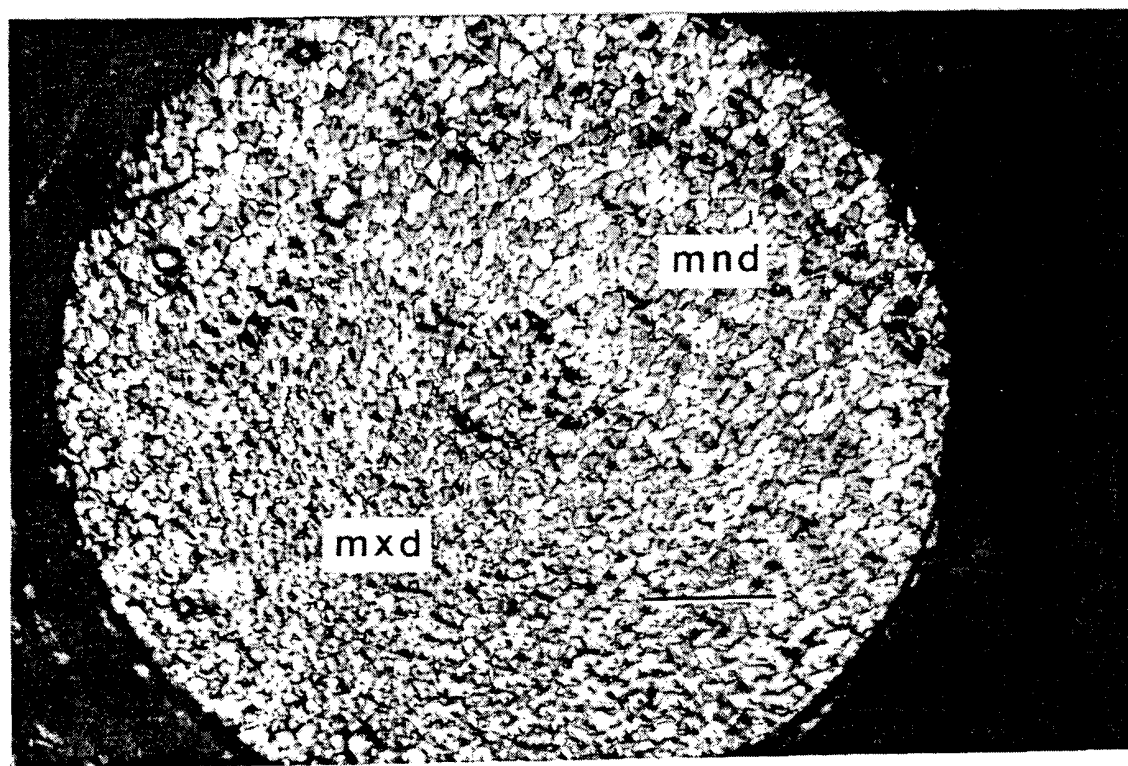
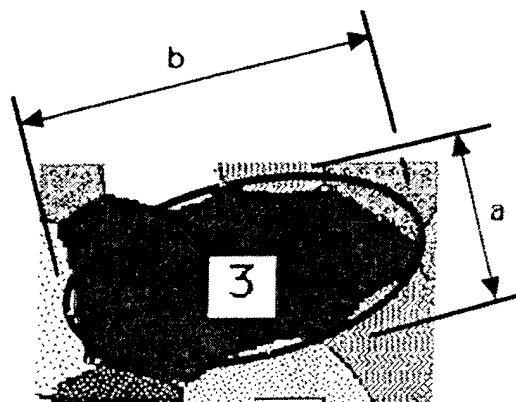
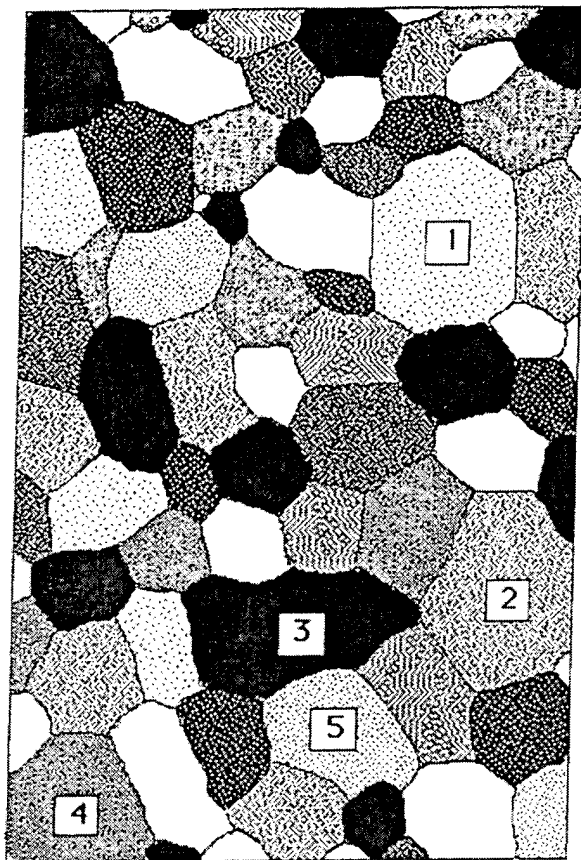


FIG. 8.1b



grain area = $0.25\pi ab$

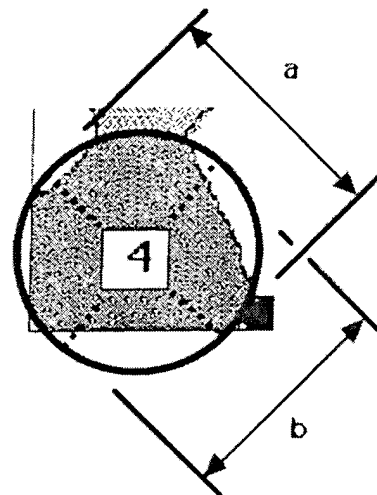
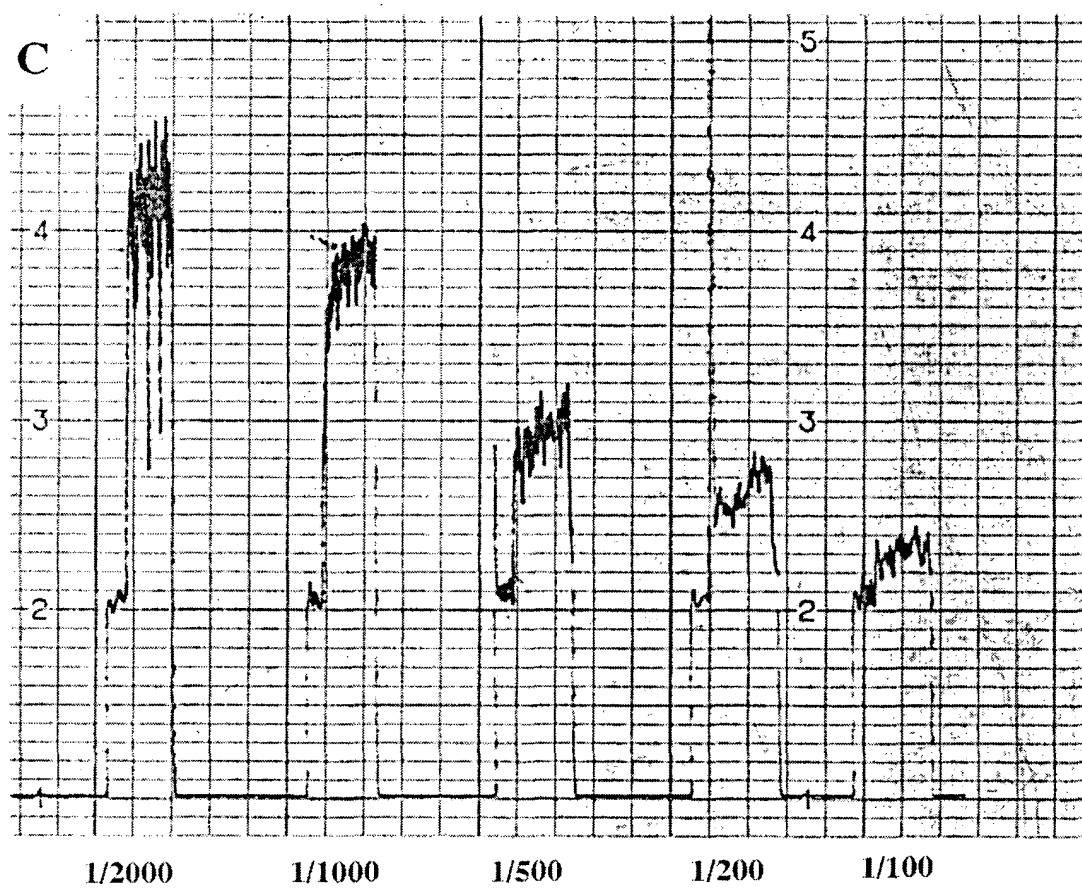
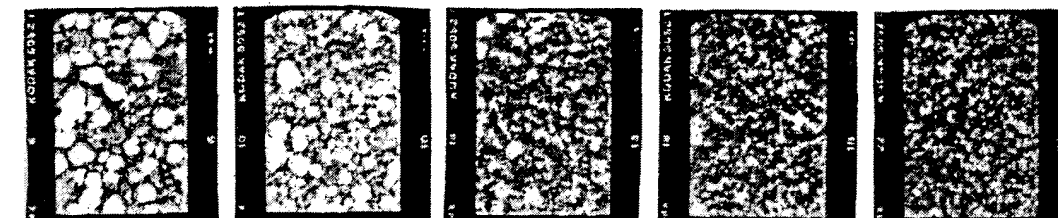


FIG. 8.2

A



B



FOI 90-96292B60

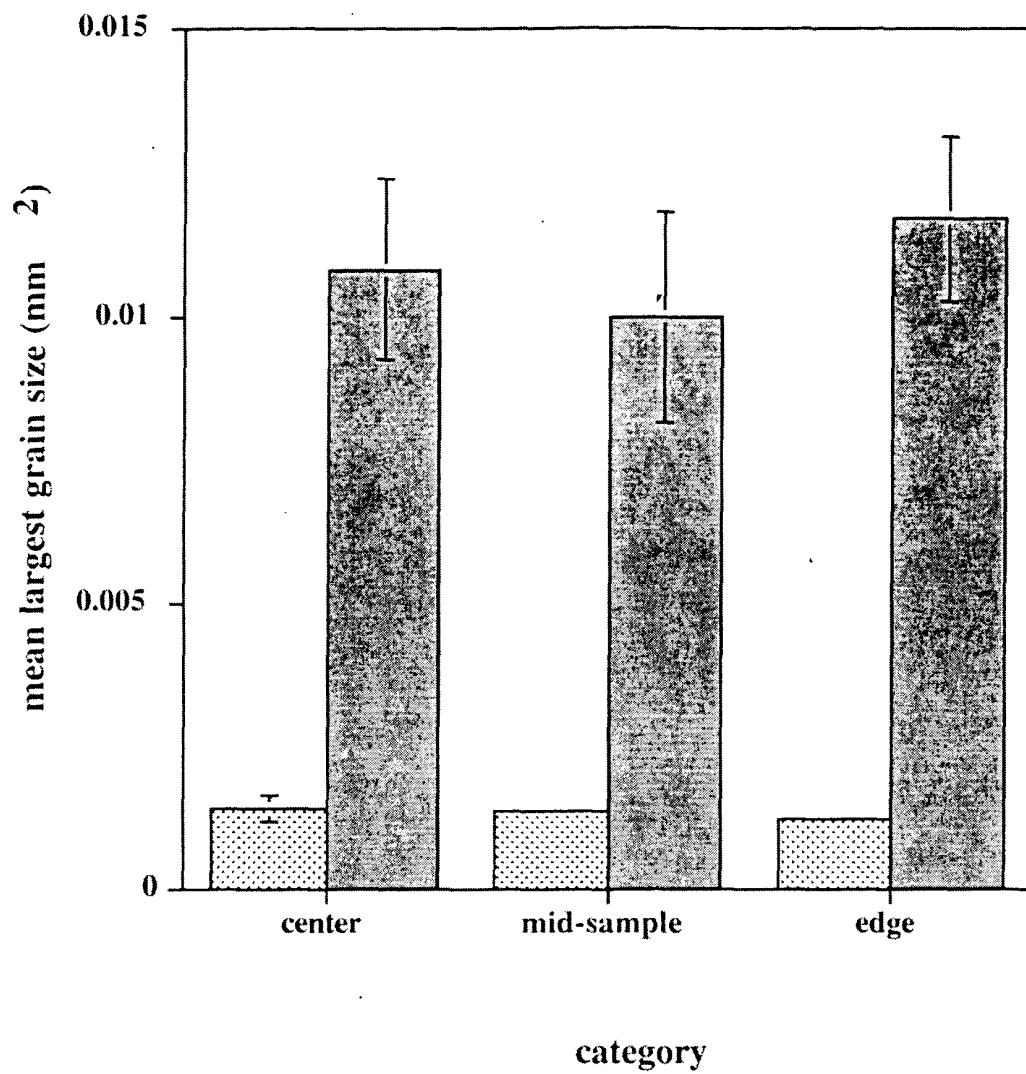


FIG. 8.4a

09876796.060701
FDZ090" 96292860

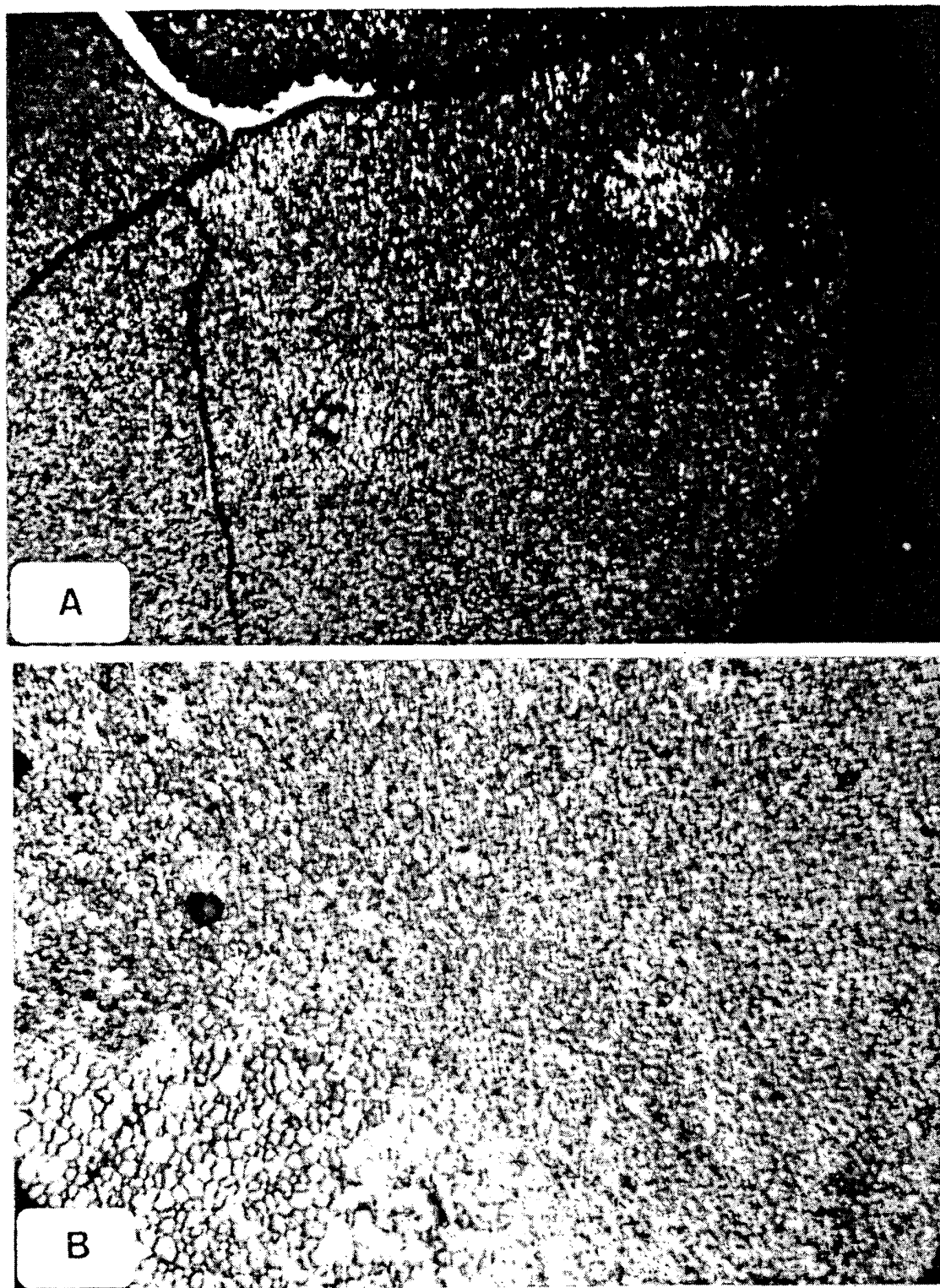


FIG. 8.4b

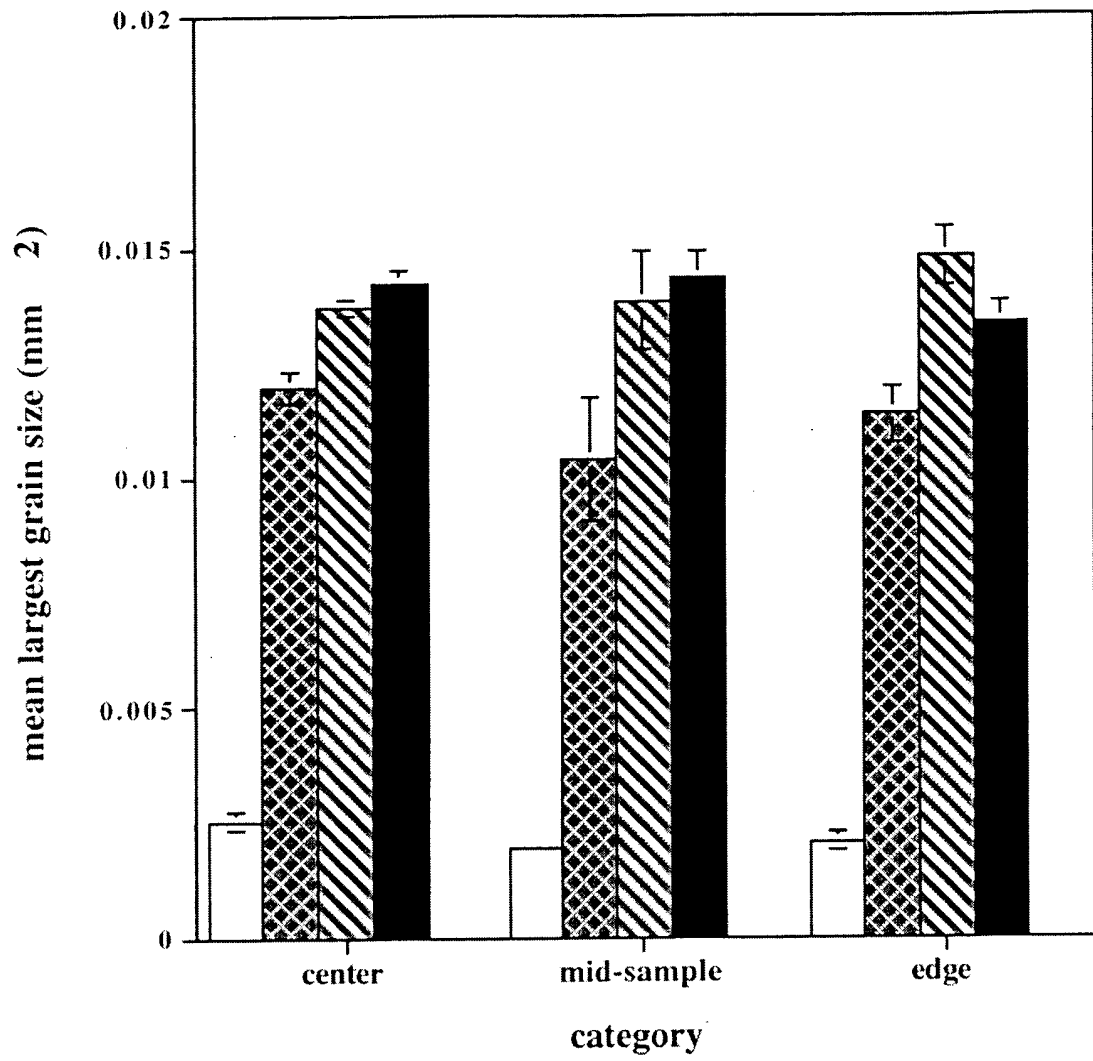


FIG. 8.5a

09876796-060701

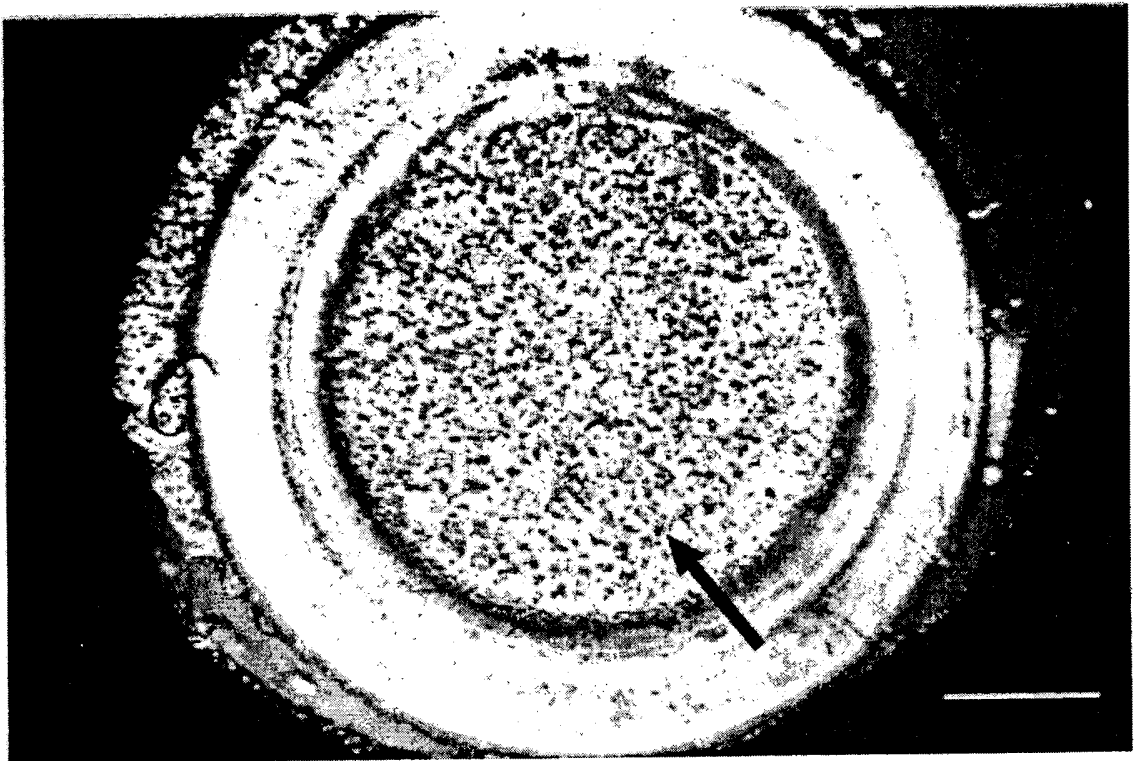


FIG. 8.5b

09876796-060701

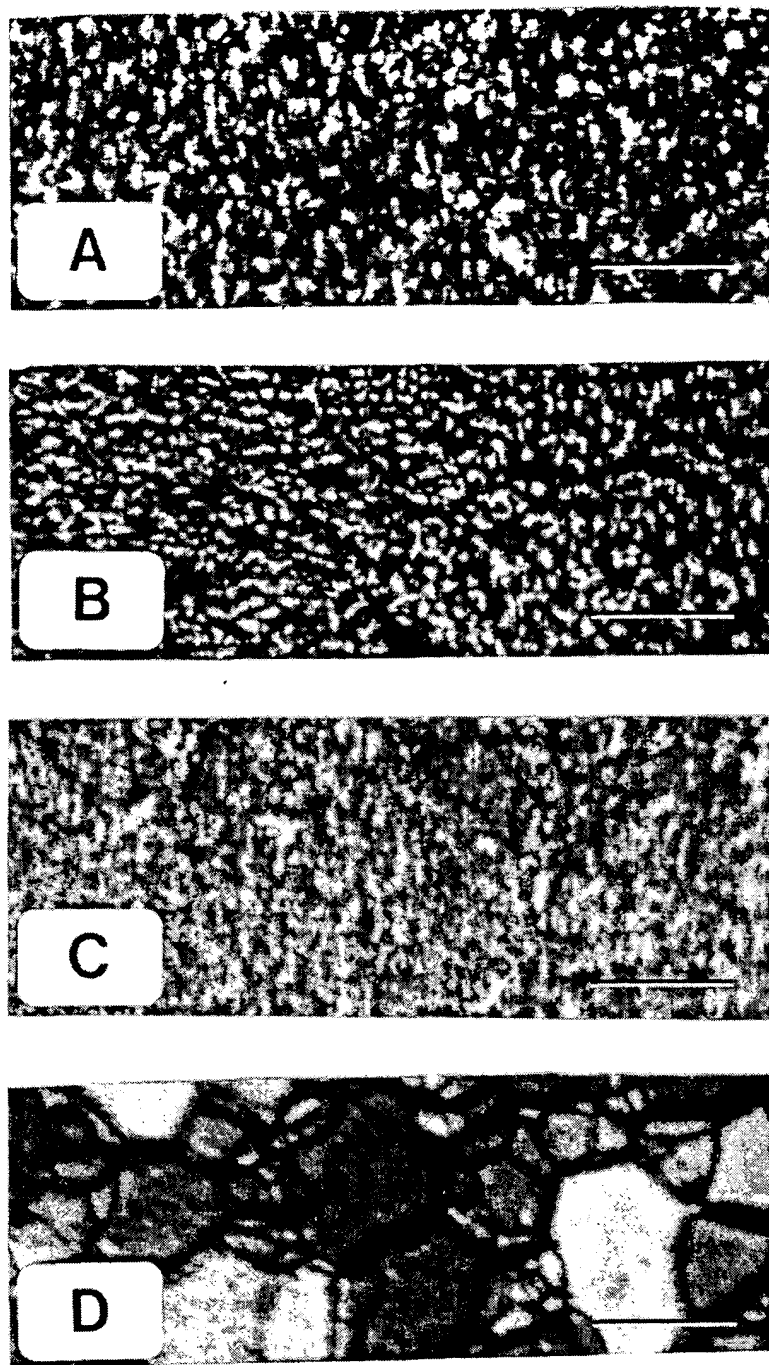


FIG. 8.6

09876796-060701

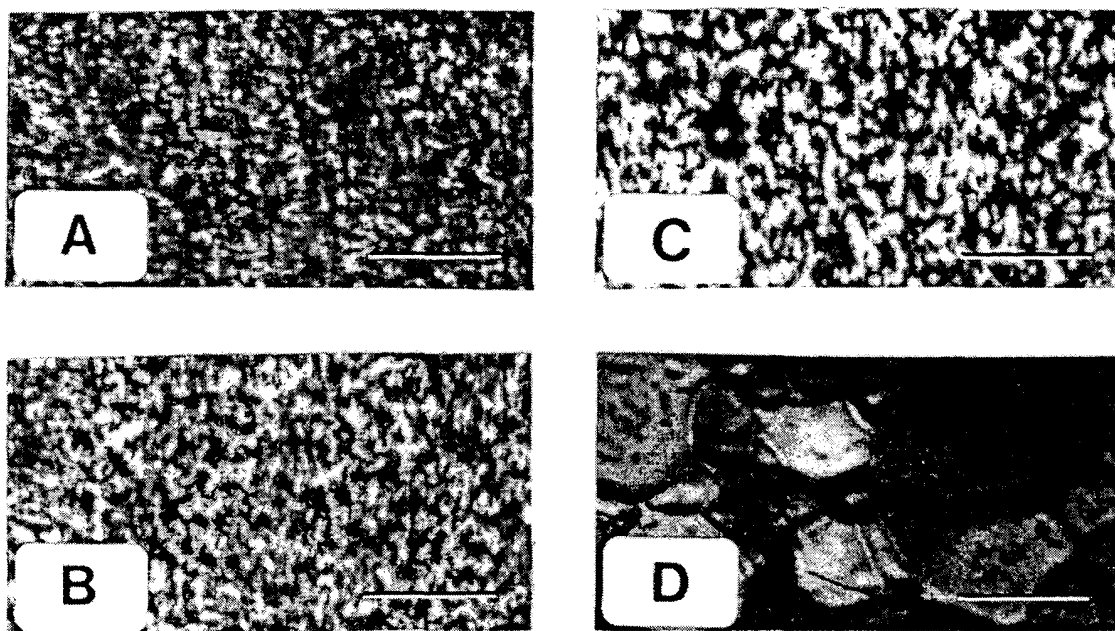


FIG. 8.7

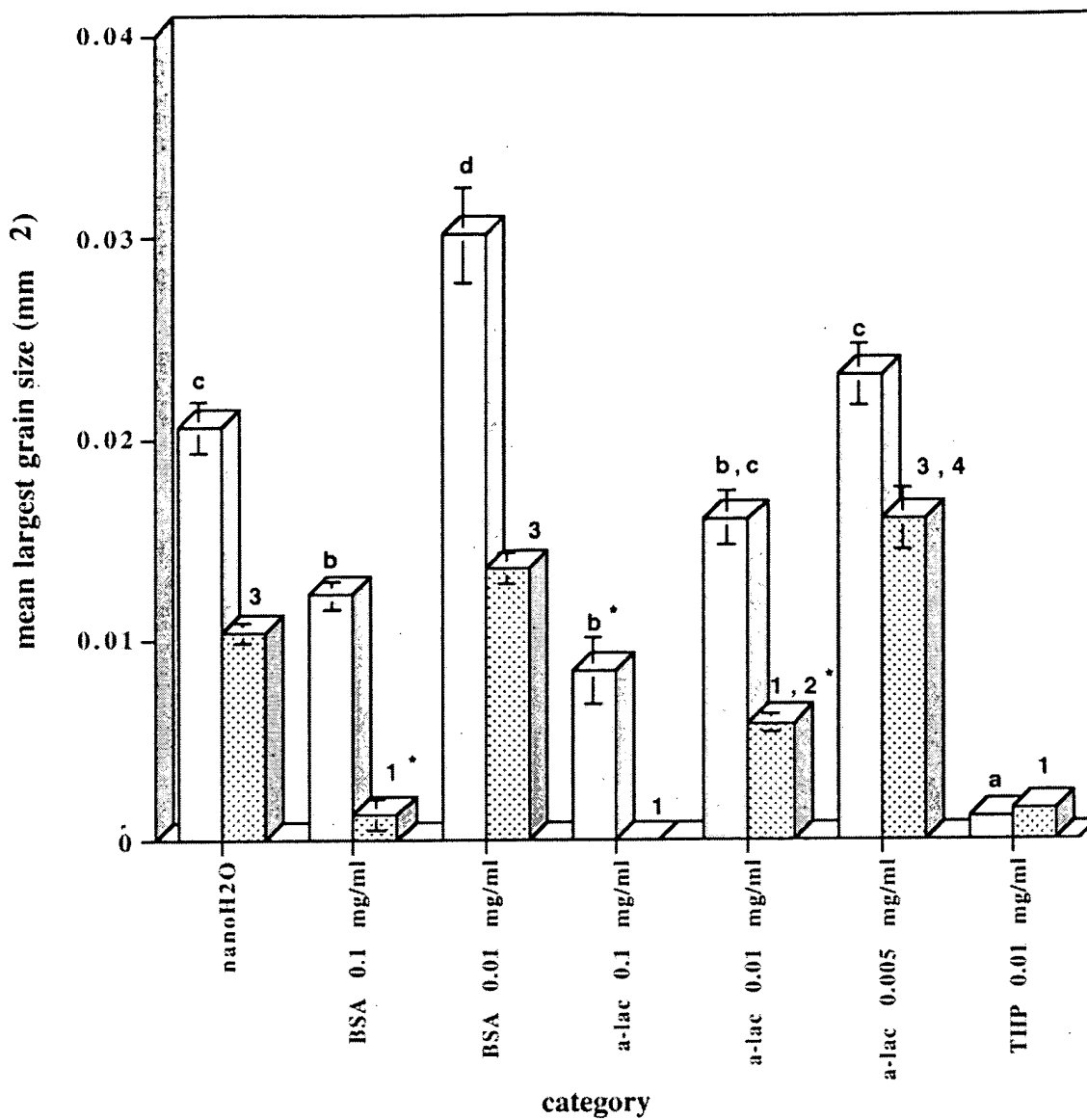


FIG. 8.8

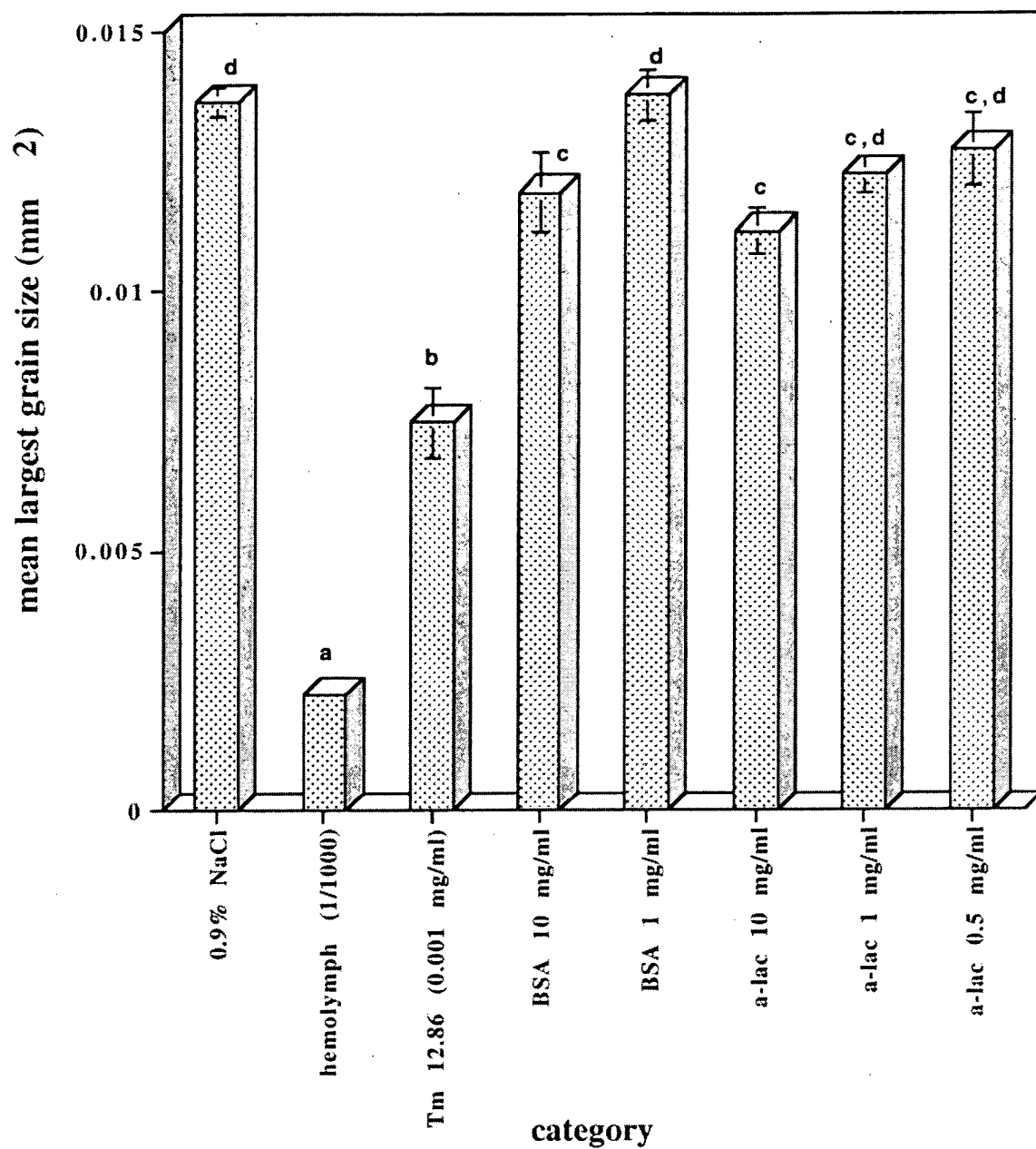


FIG. 8.9

00876796-060701

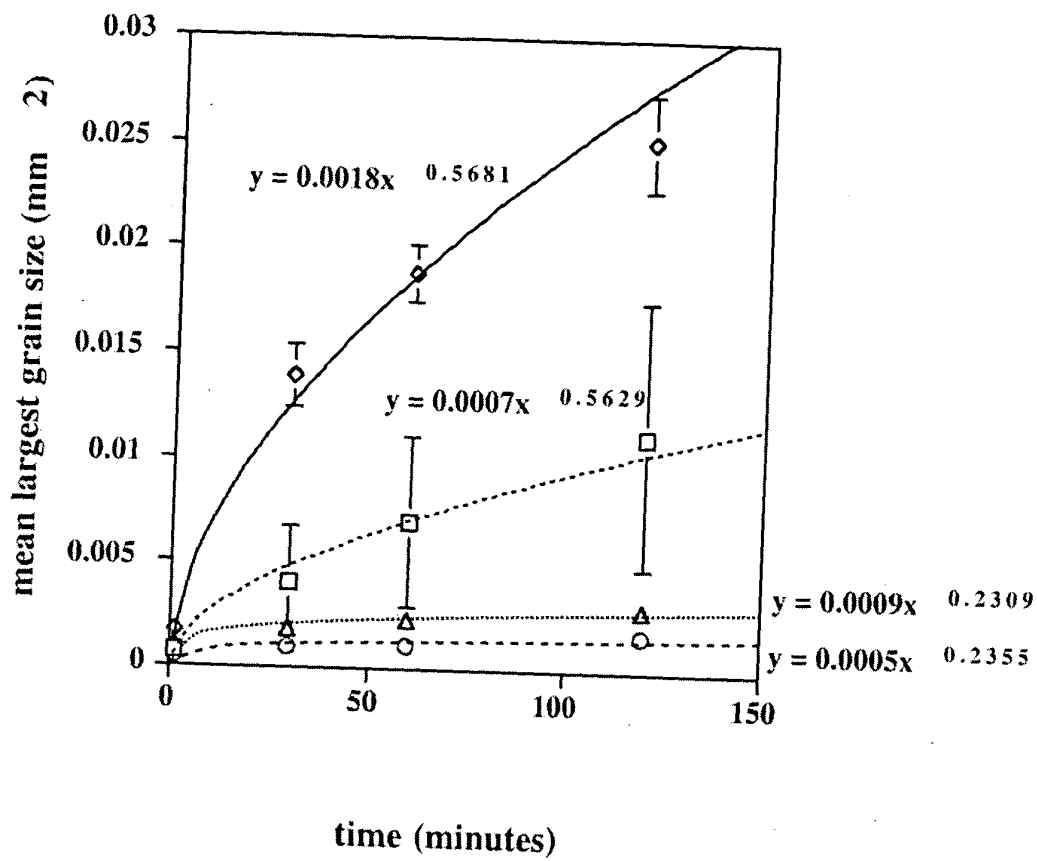


FIG. 8.10

104090-96292850

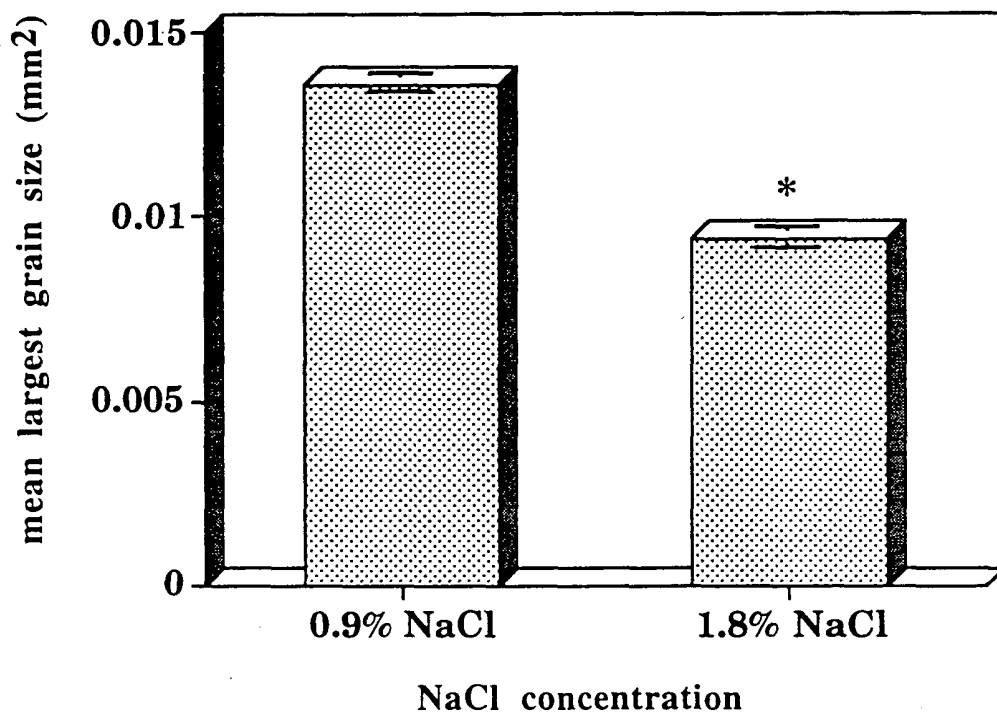


FIG. 8.11

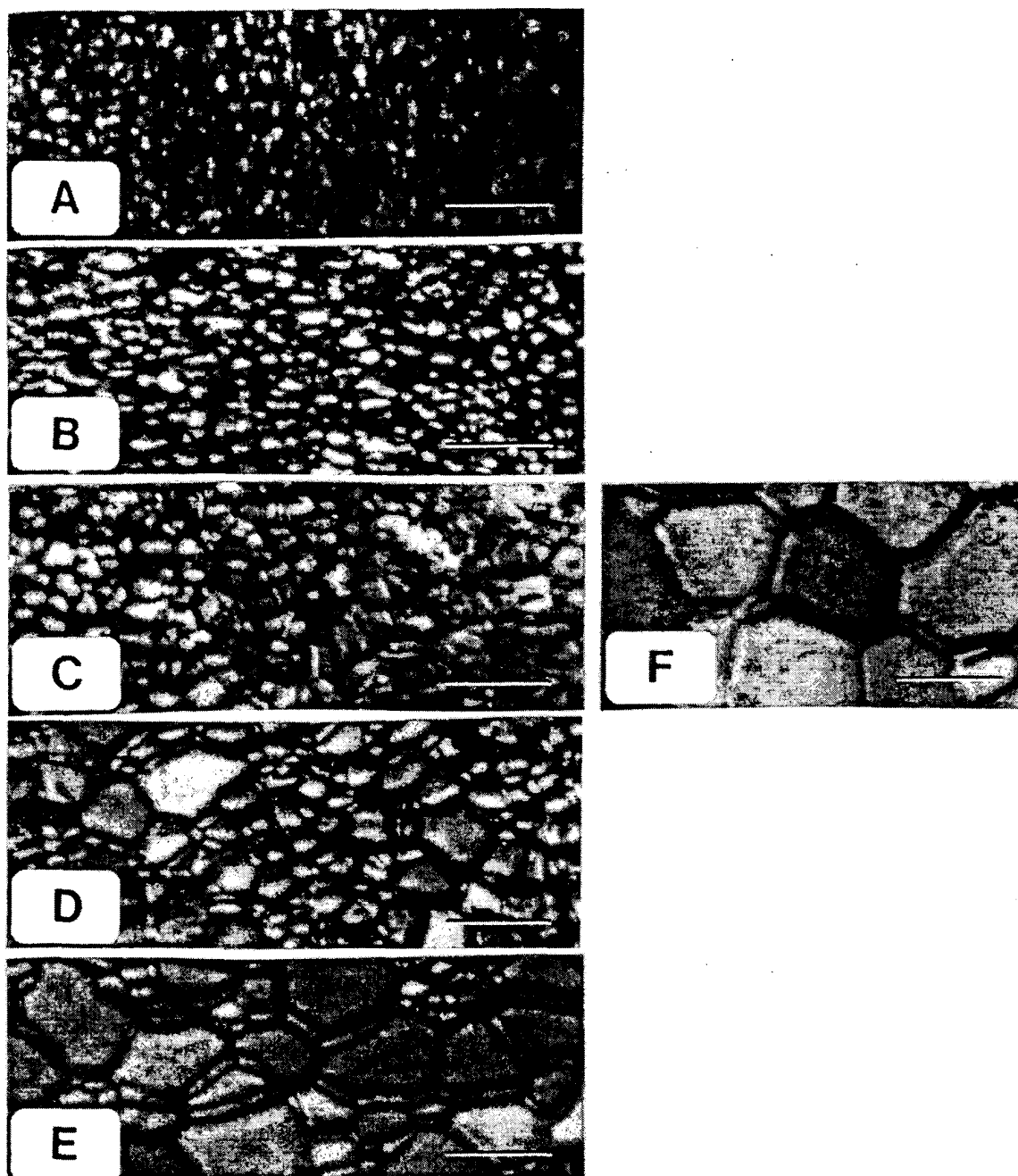


FIG. 8.12

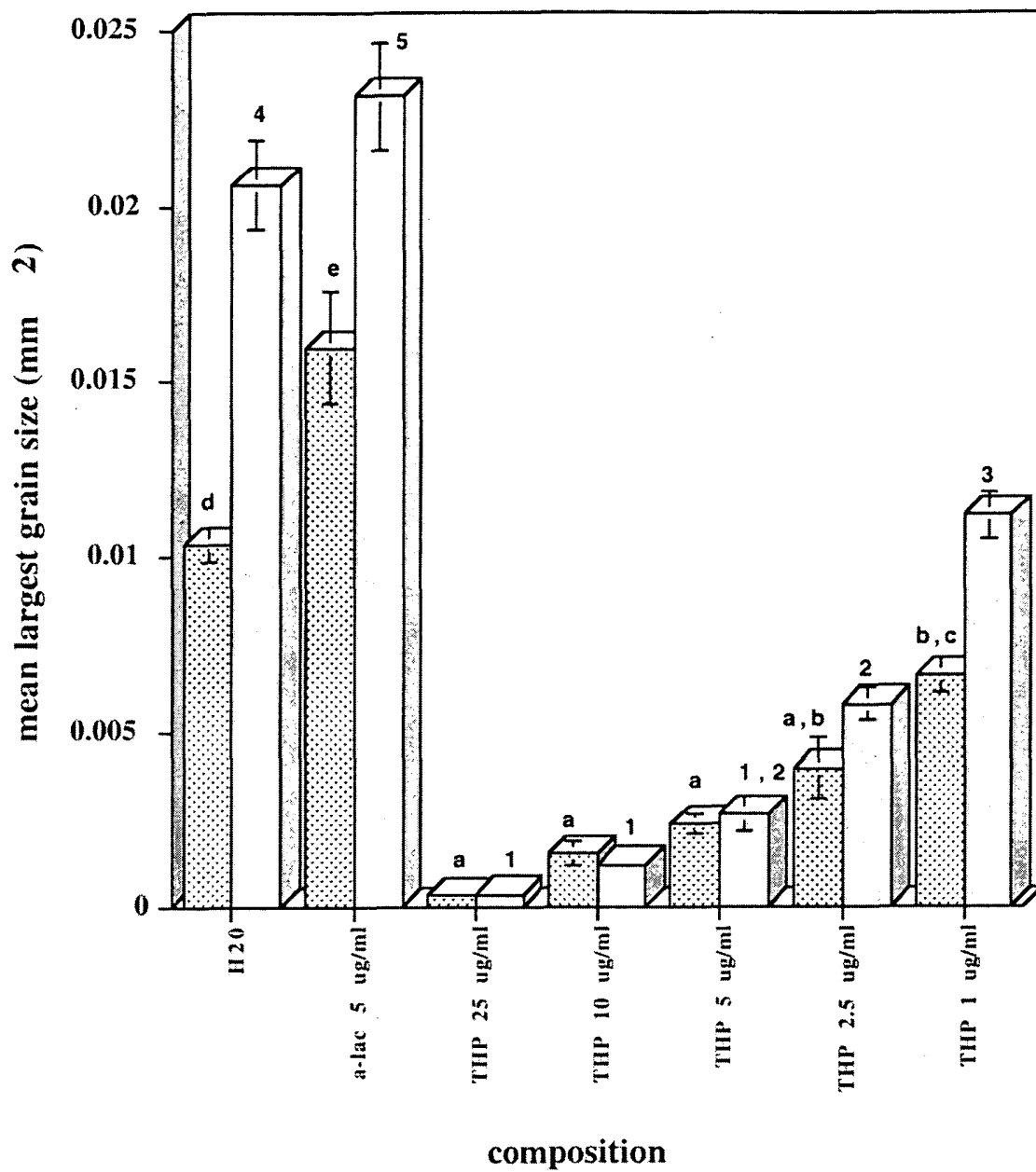


FIG. 8.13

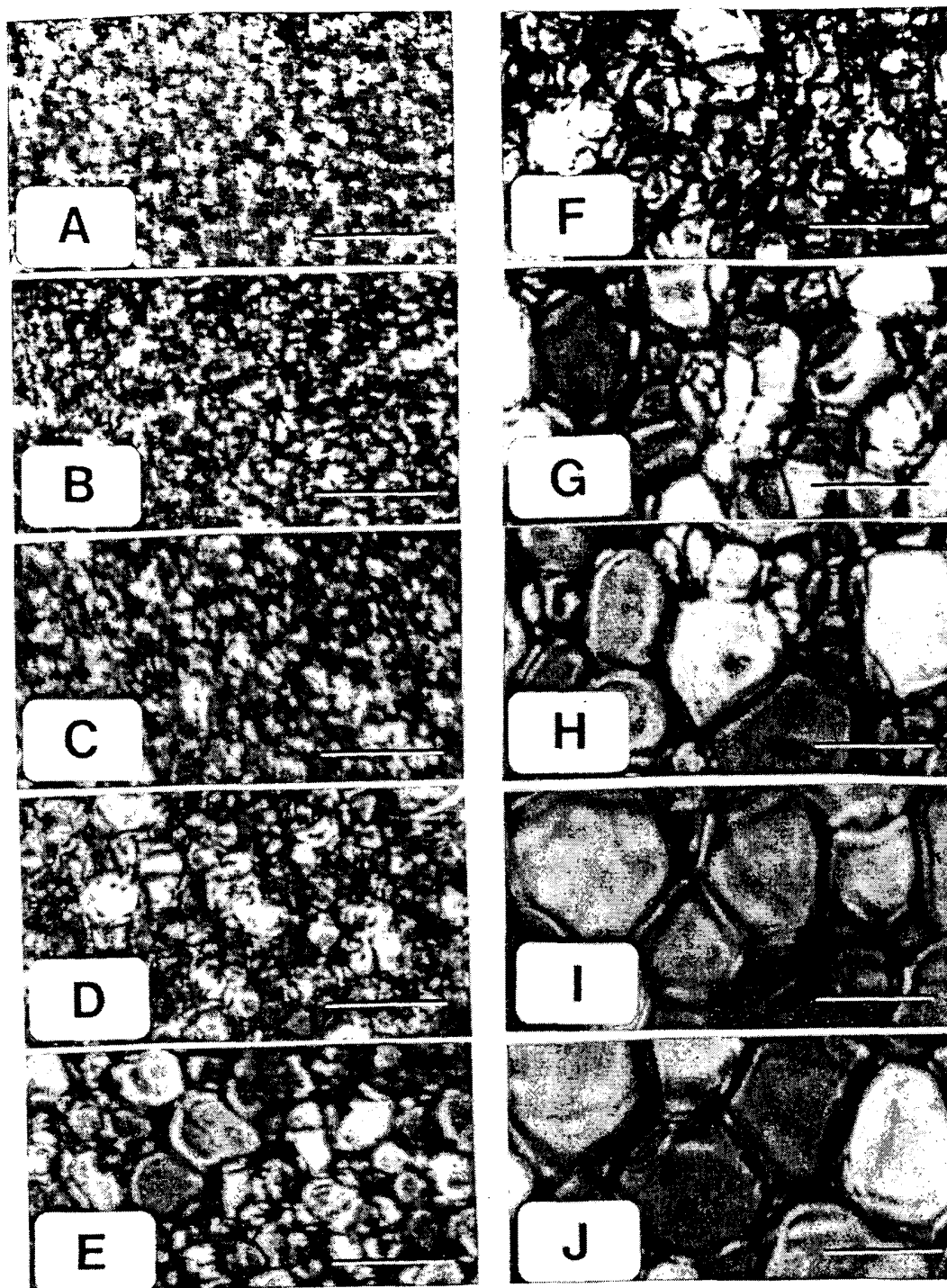


FIG. 8.14

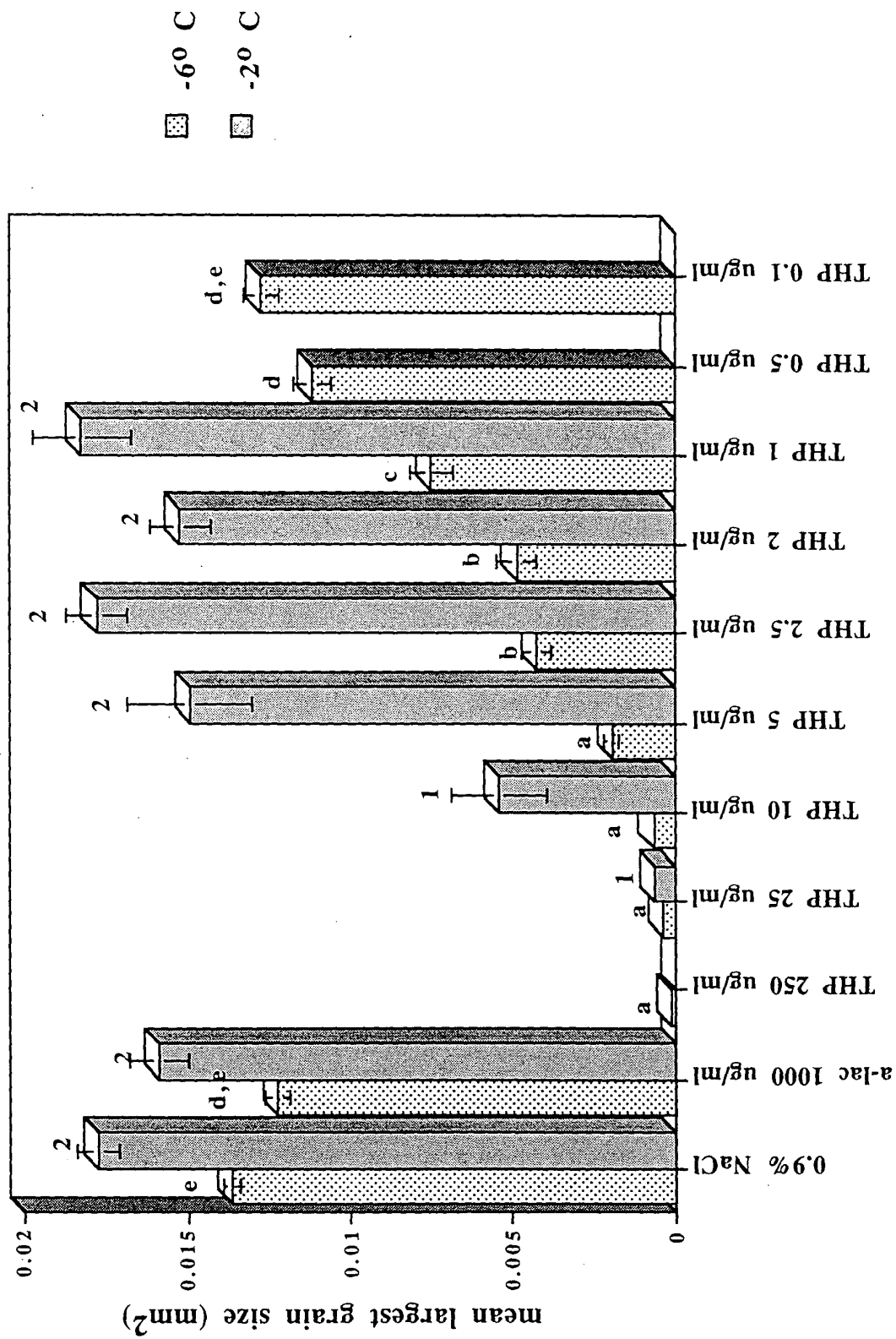


FIG. 8.15

704090-96292860

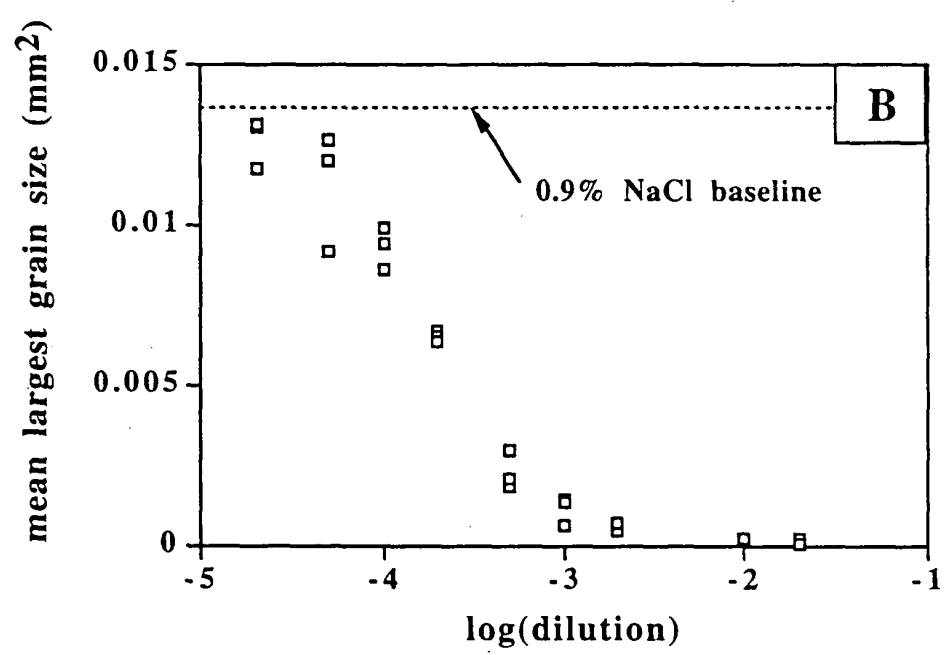
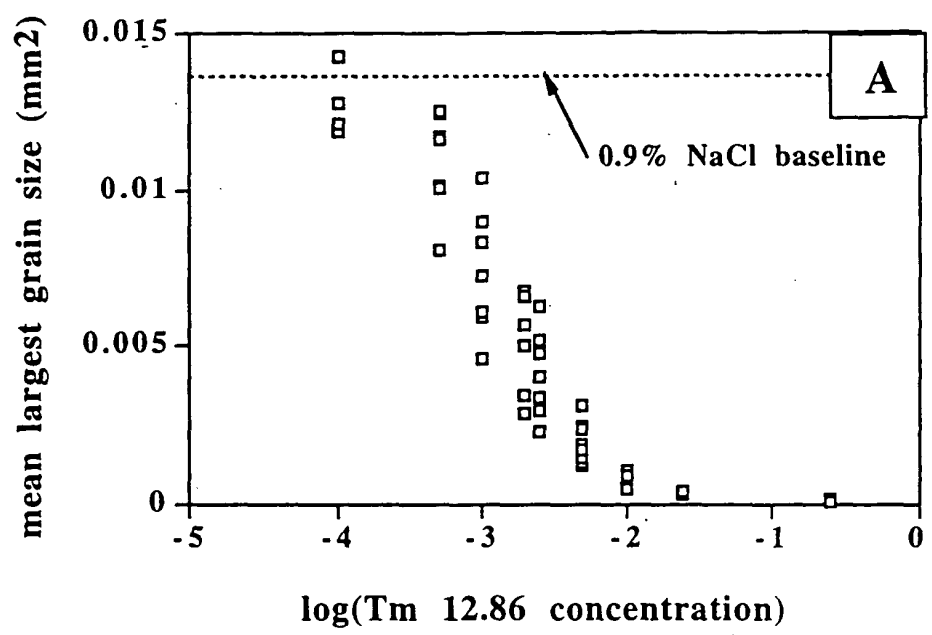


FIG. 8.16

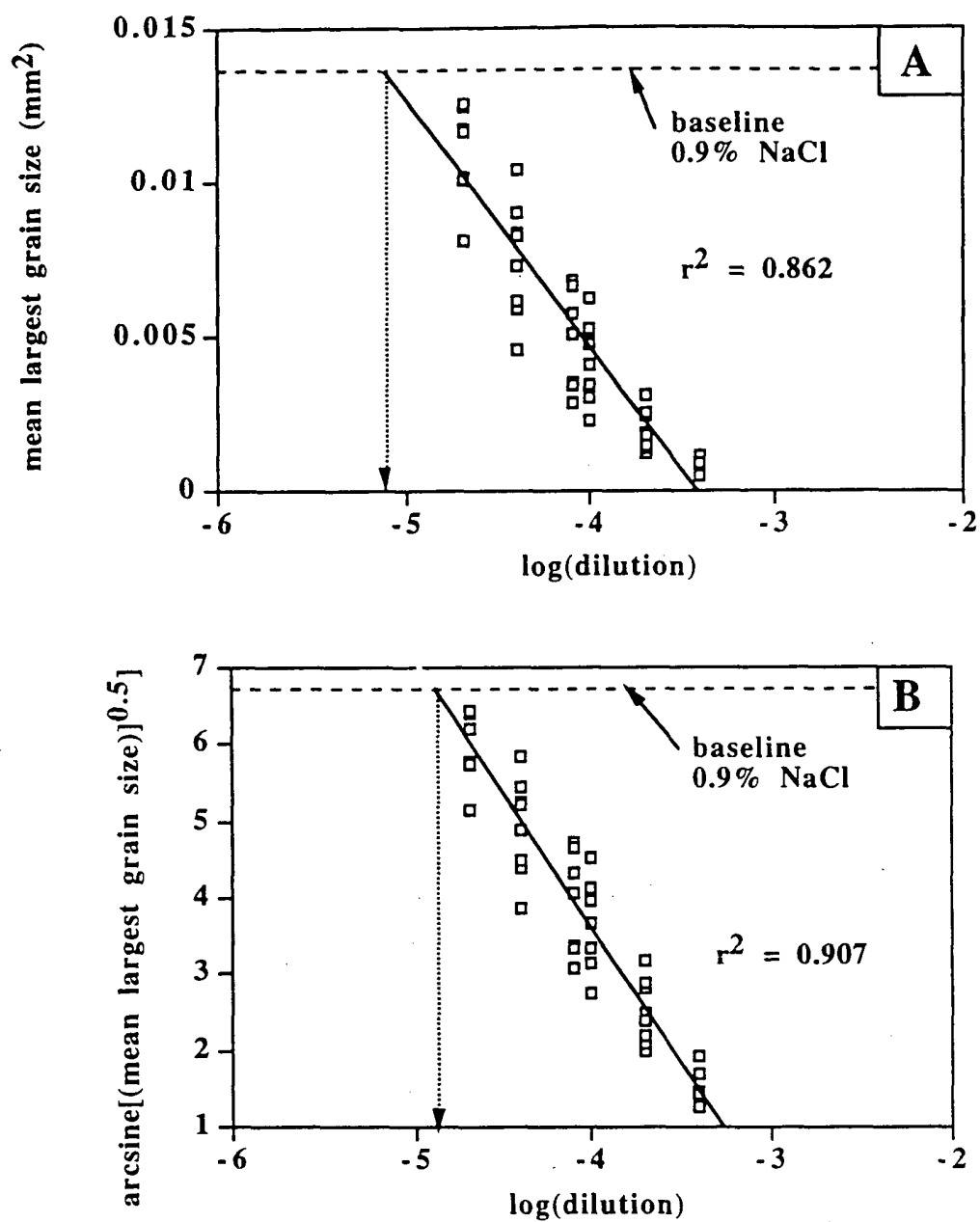


FIG. 8.17

096796-060701
T04090" 95494850

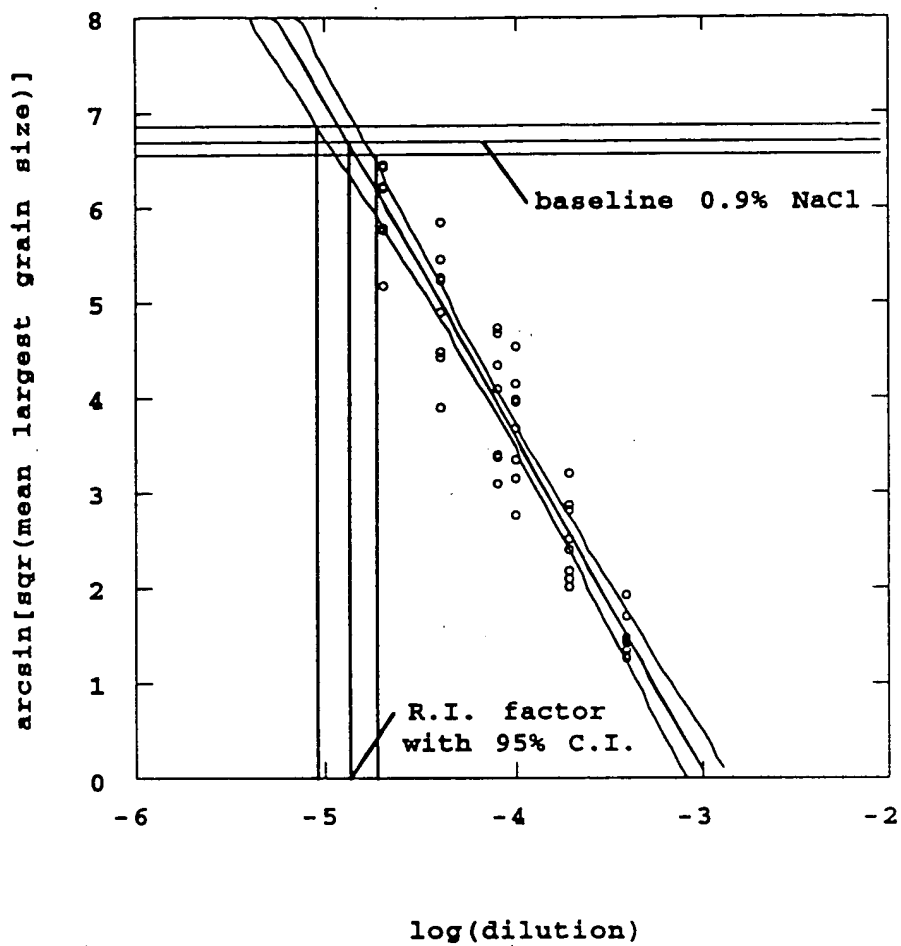


FIG. 8.18

FD2090" 96292860

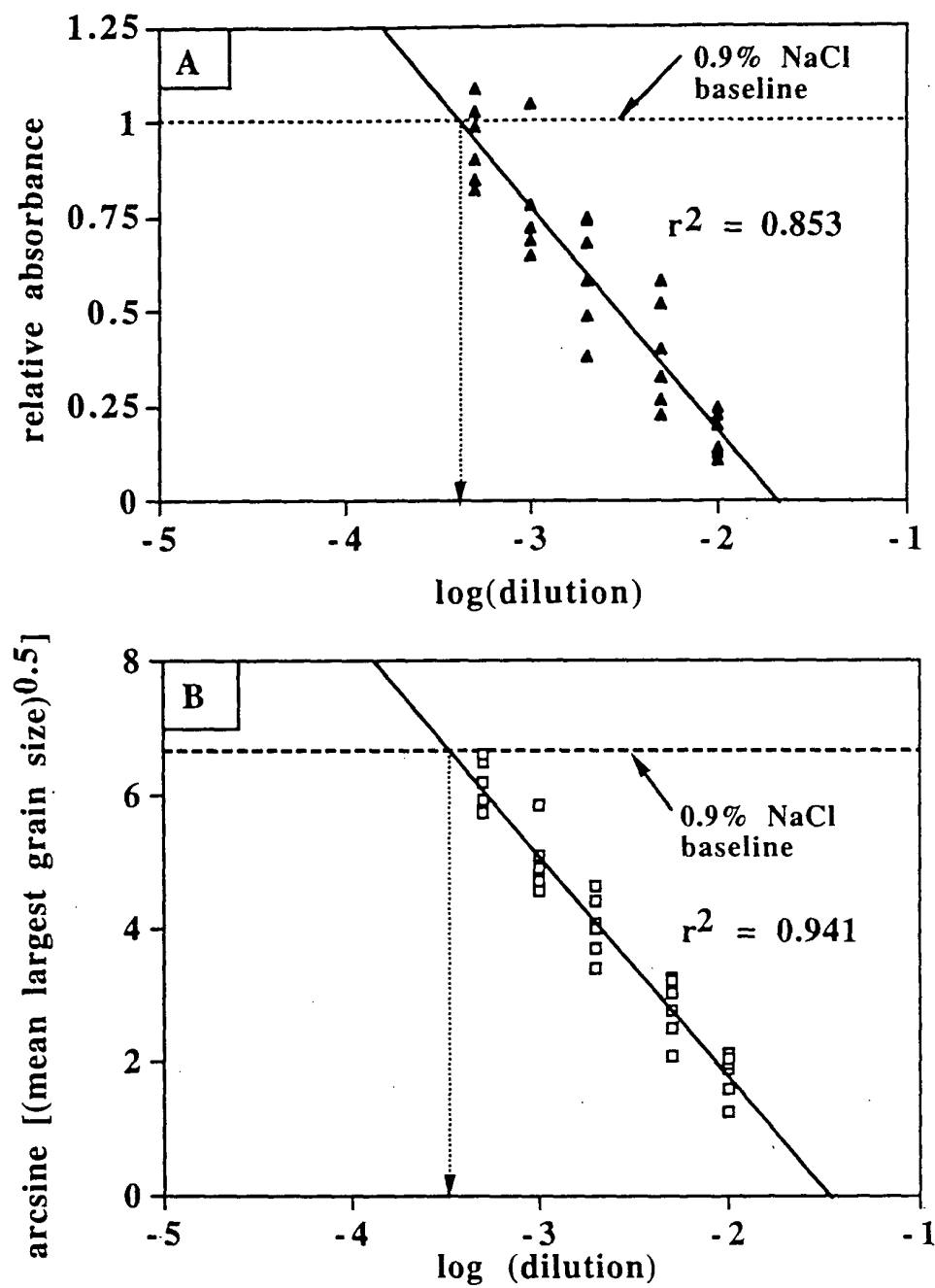


FIG. 8.19

102090-96292860

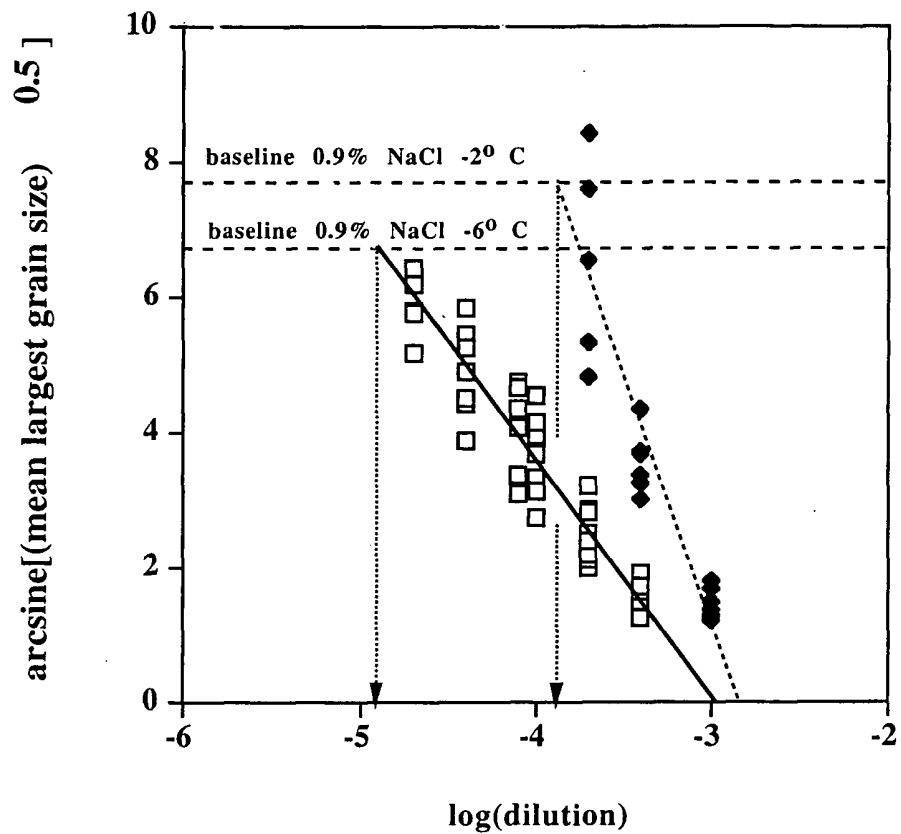


FIG. 8.20

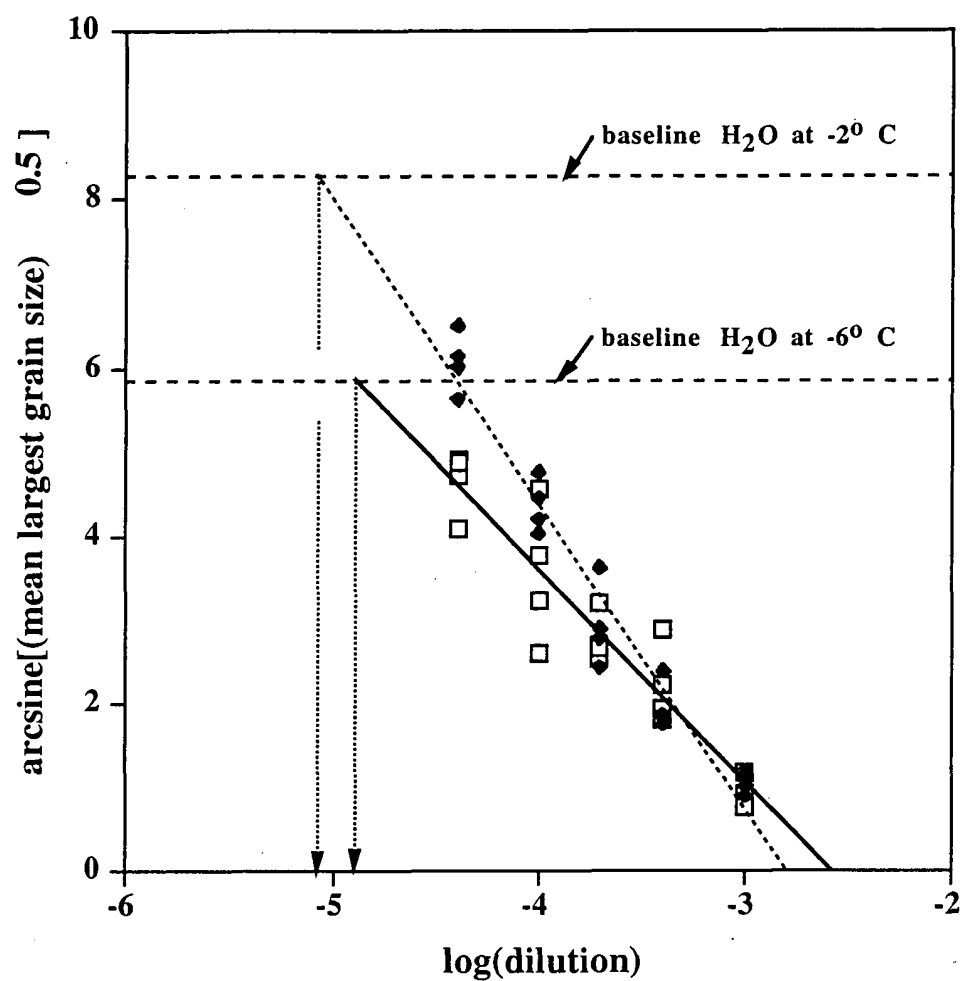


FIG. 8.21

096795 096795 096795

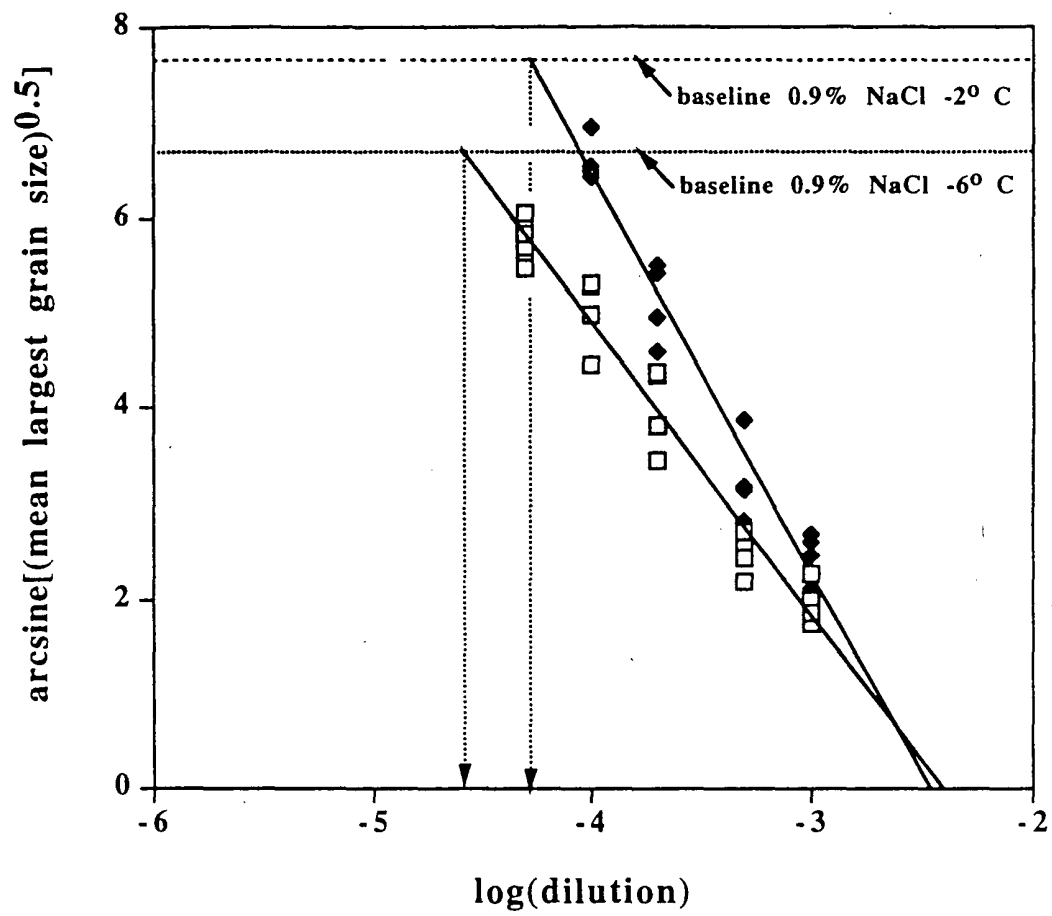


FIG. 8.22

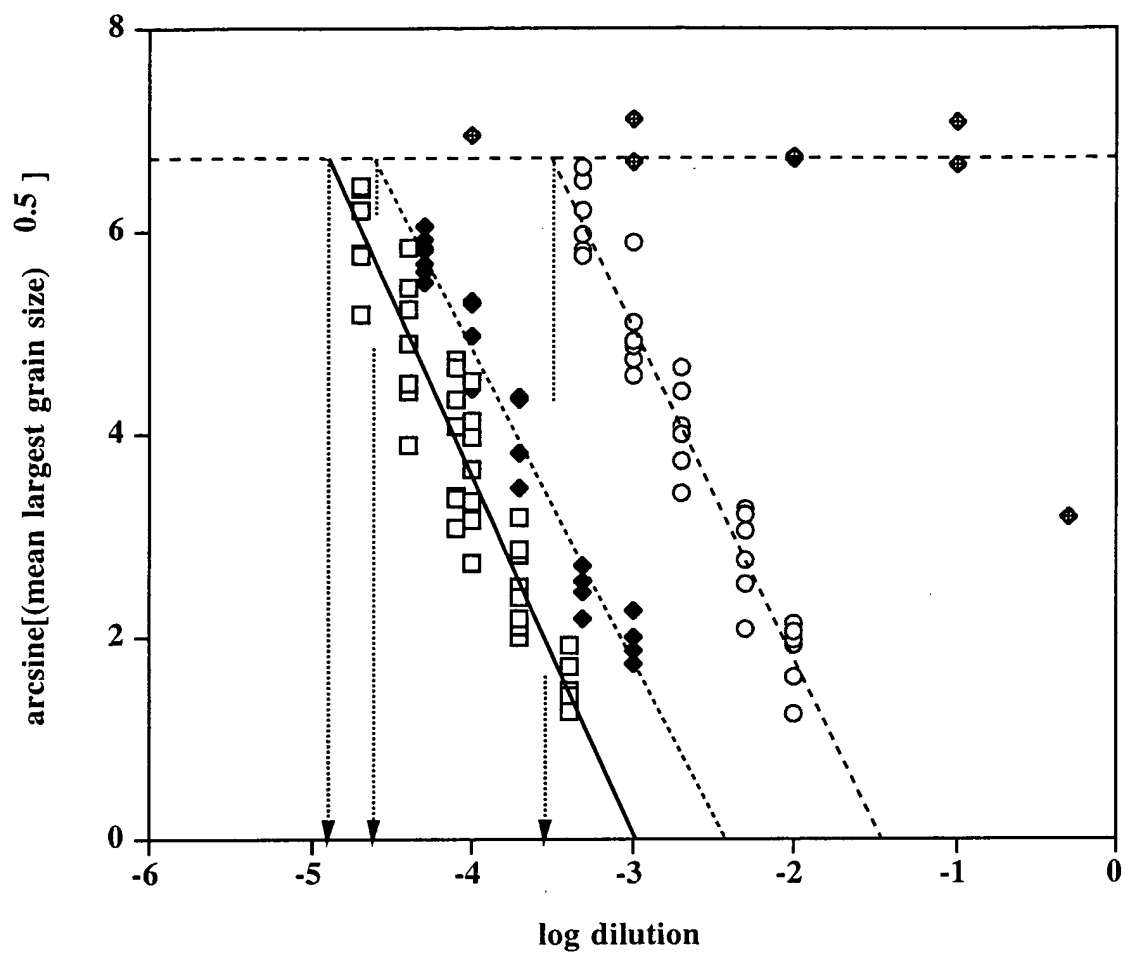


FIG. 8.23

704090-9694860

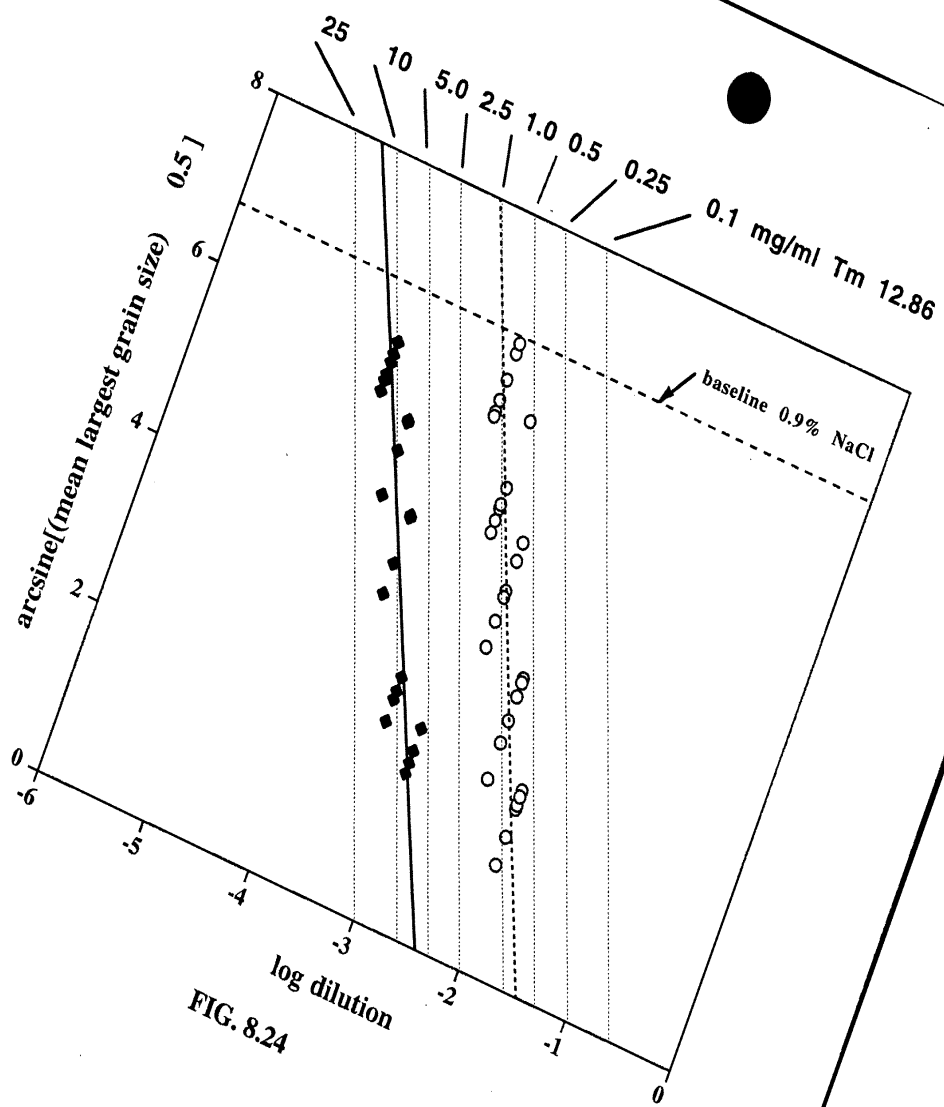


FIG. 8.24

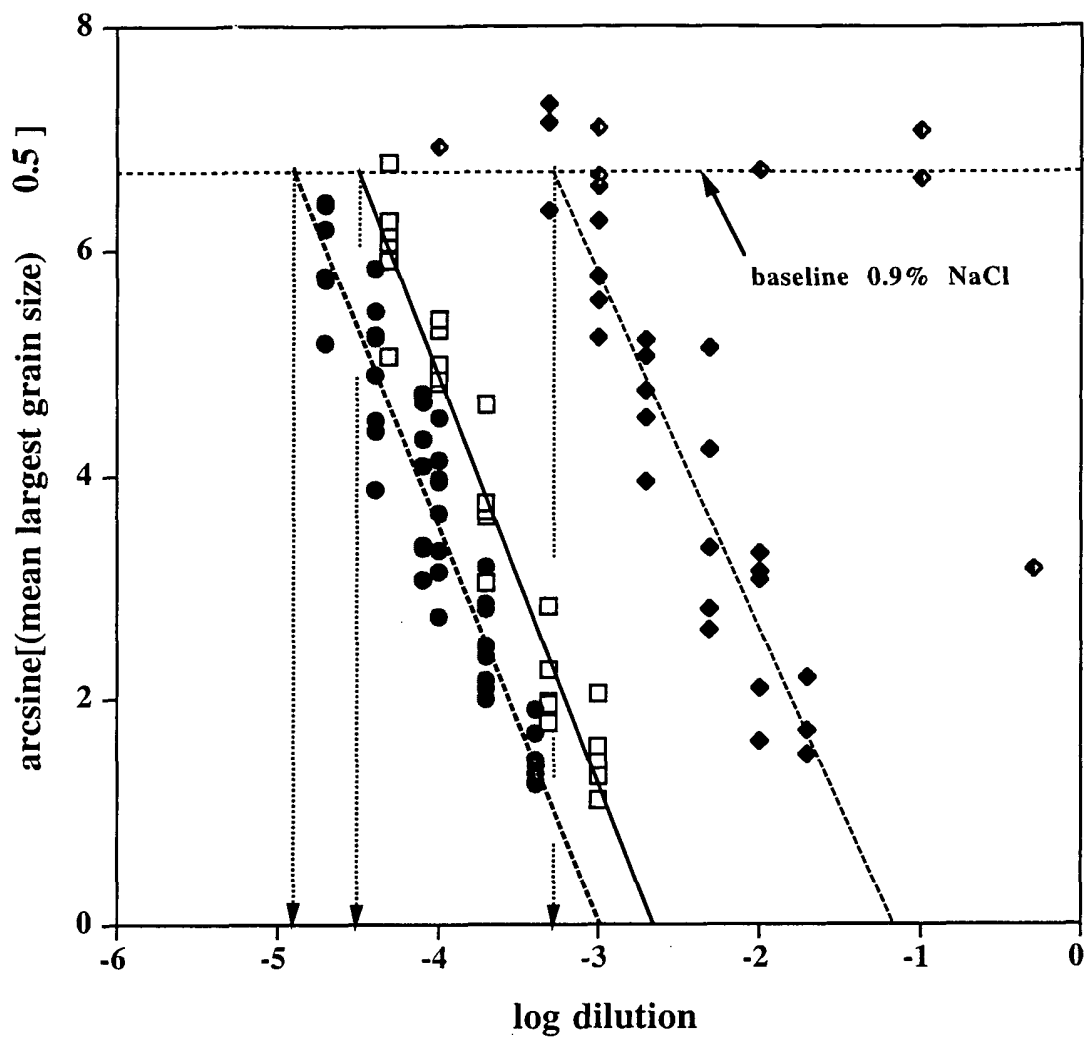


FIG. 8.25

FOC050-36292860

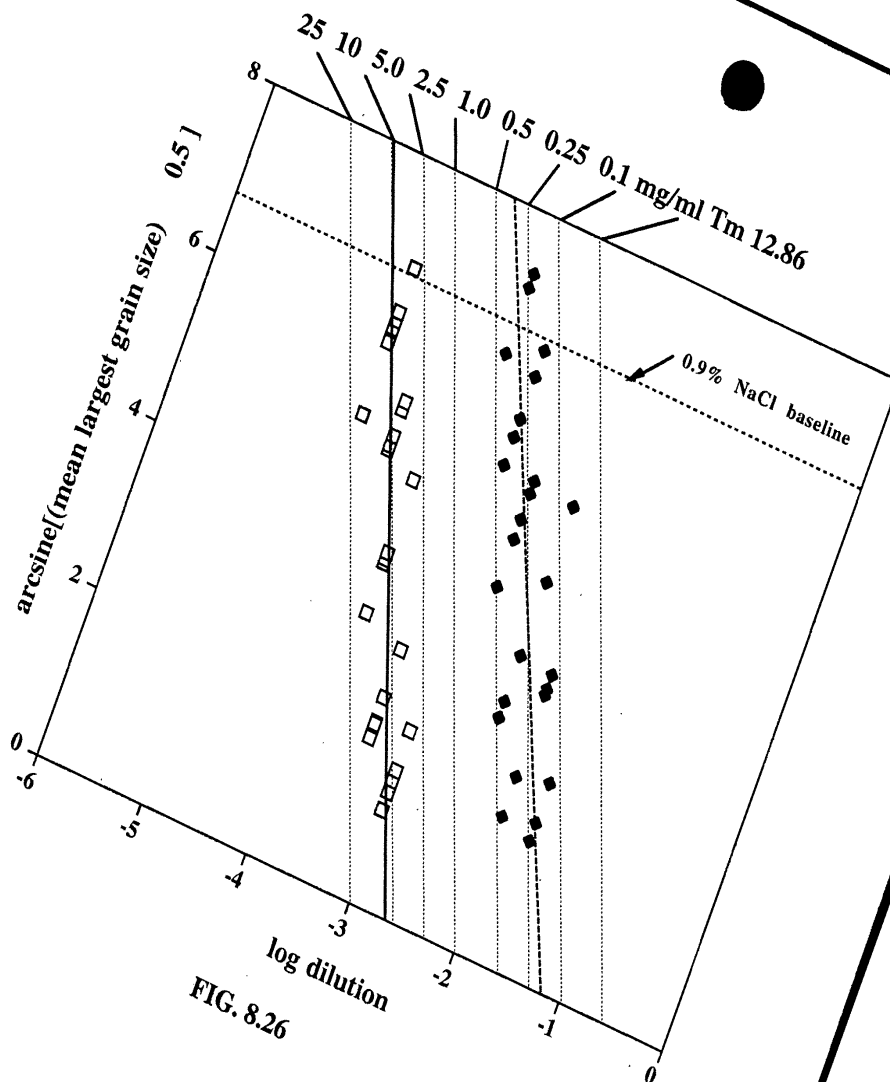


FIG. 8.26

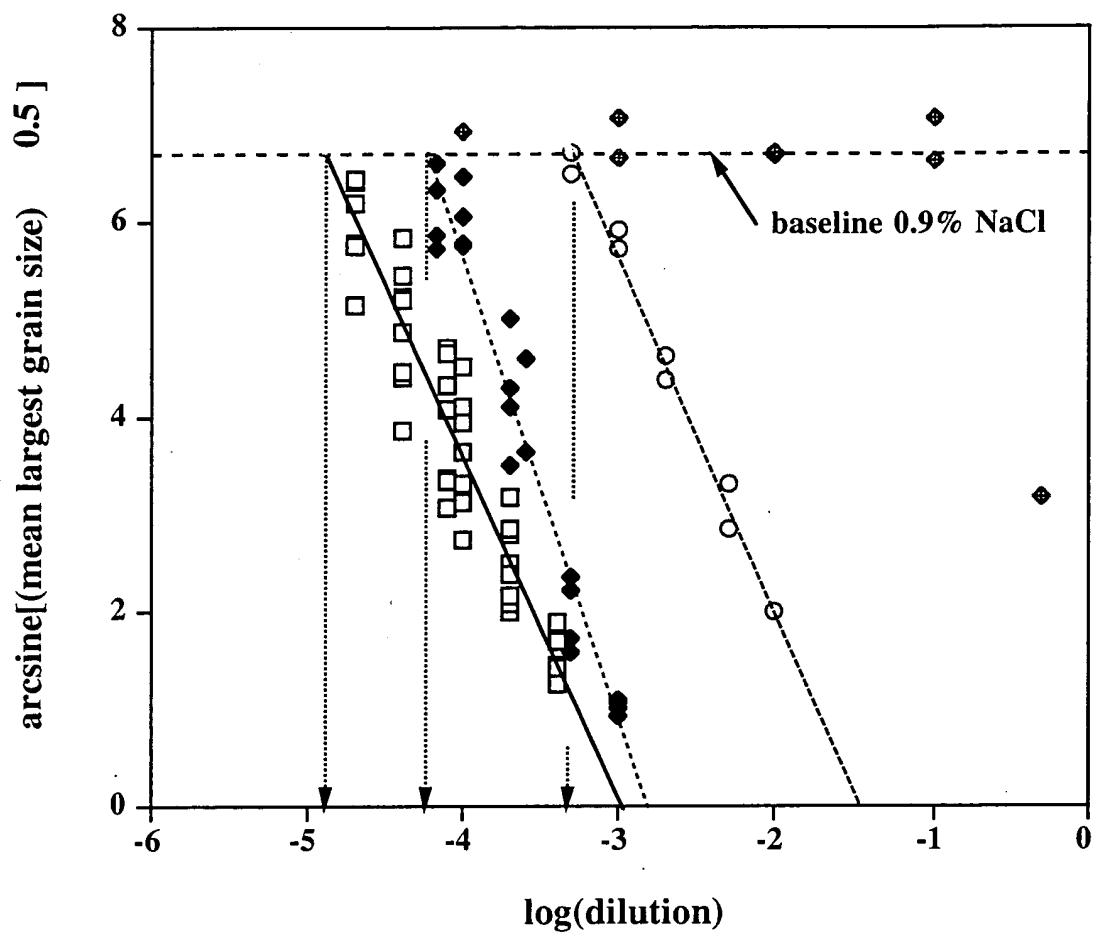


FIG. 8.27

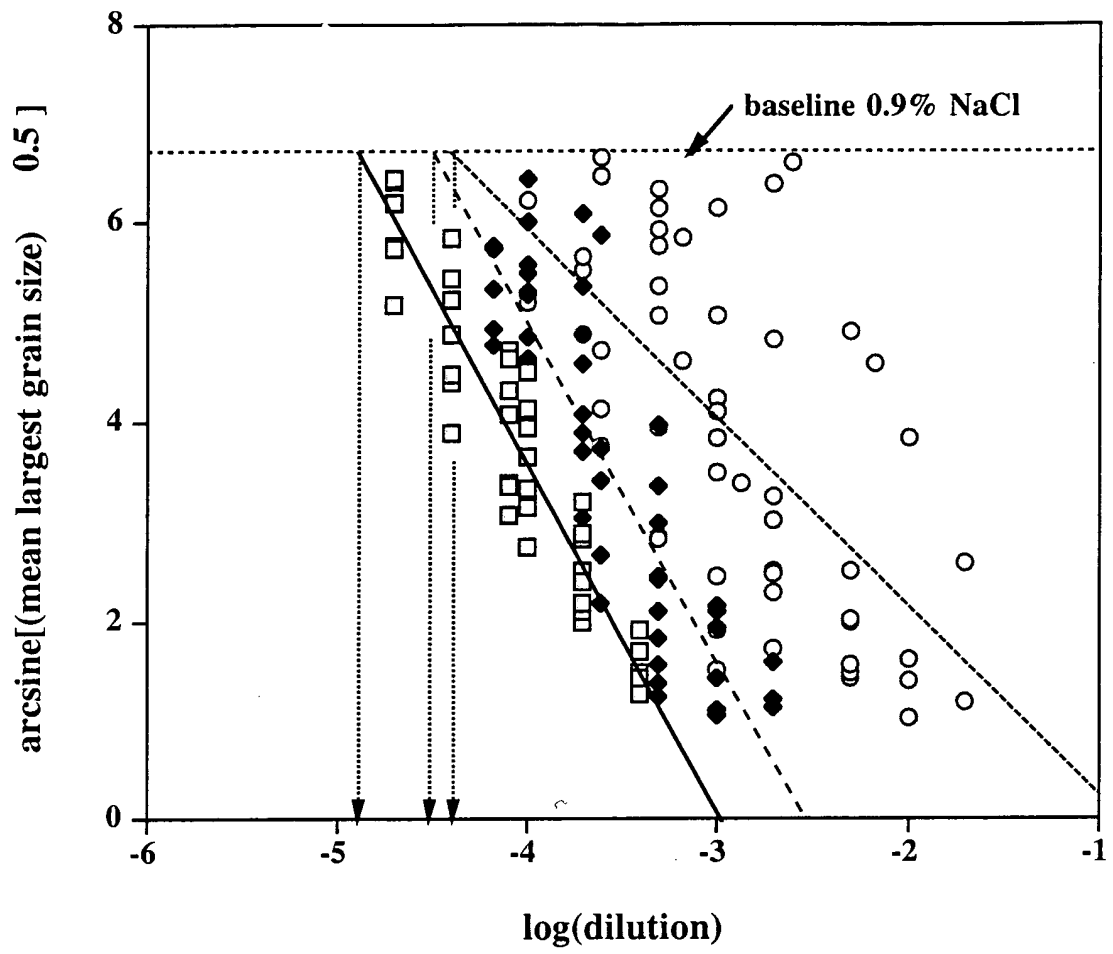


FIG. 8.28

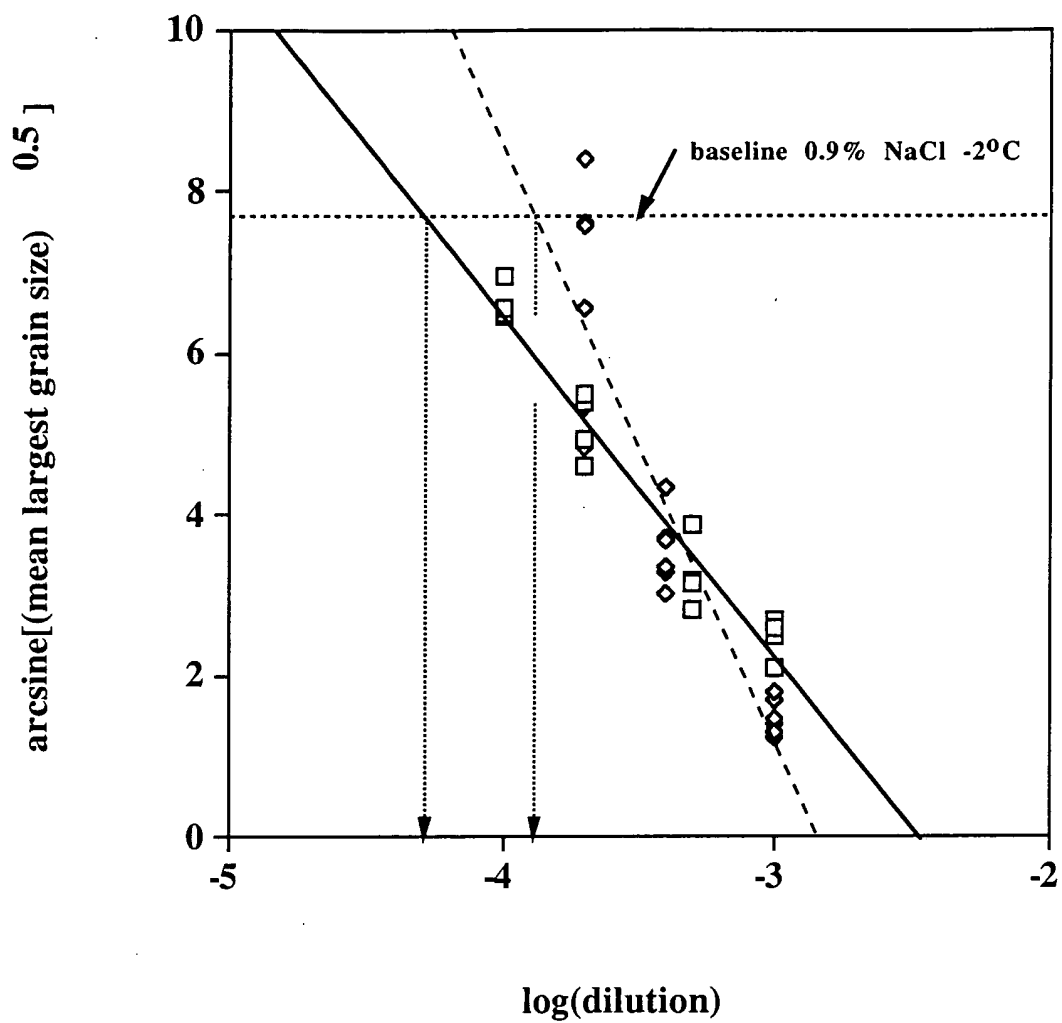


FIG. 8.29

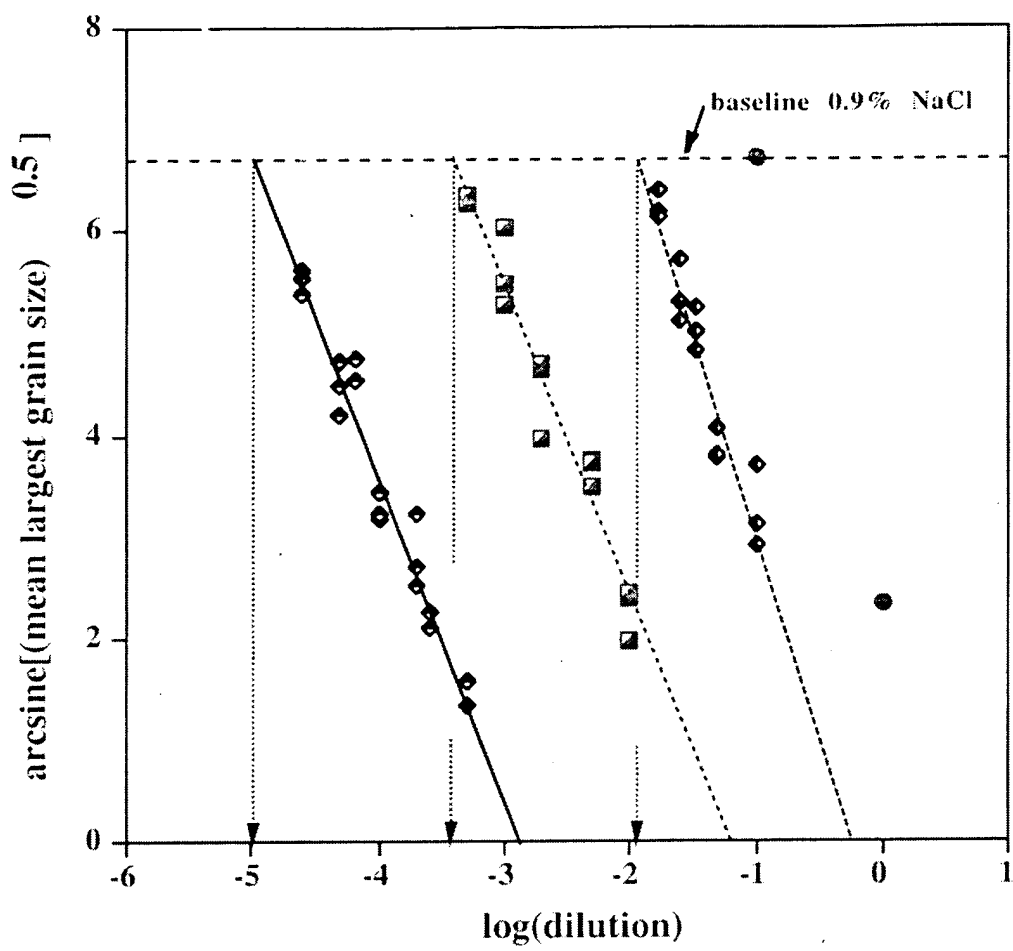


FIG. 8.30

95292860

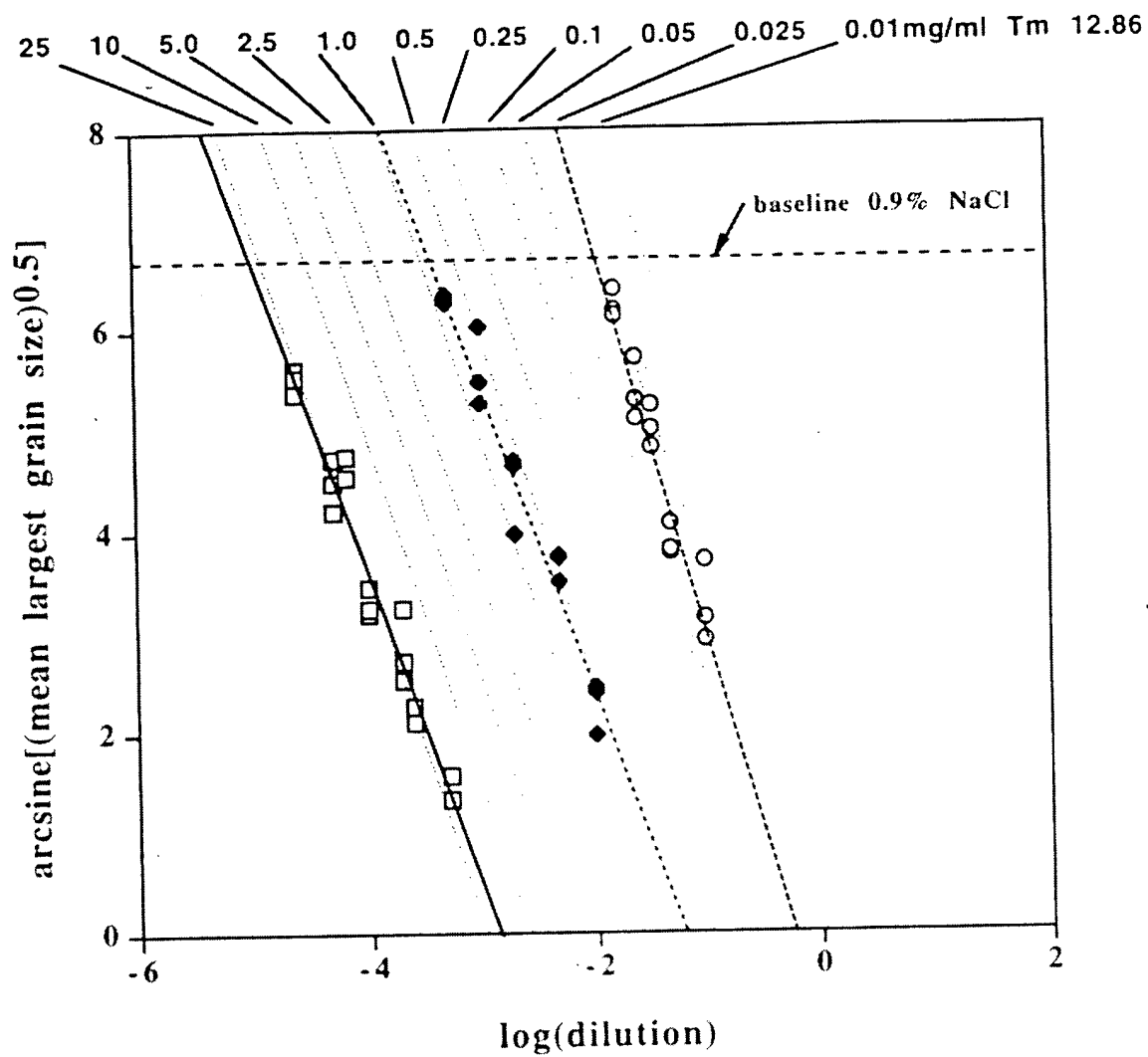


FIG. 8.31

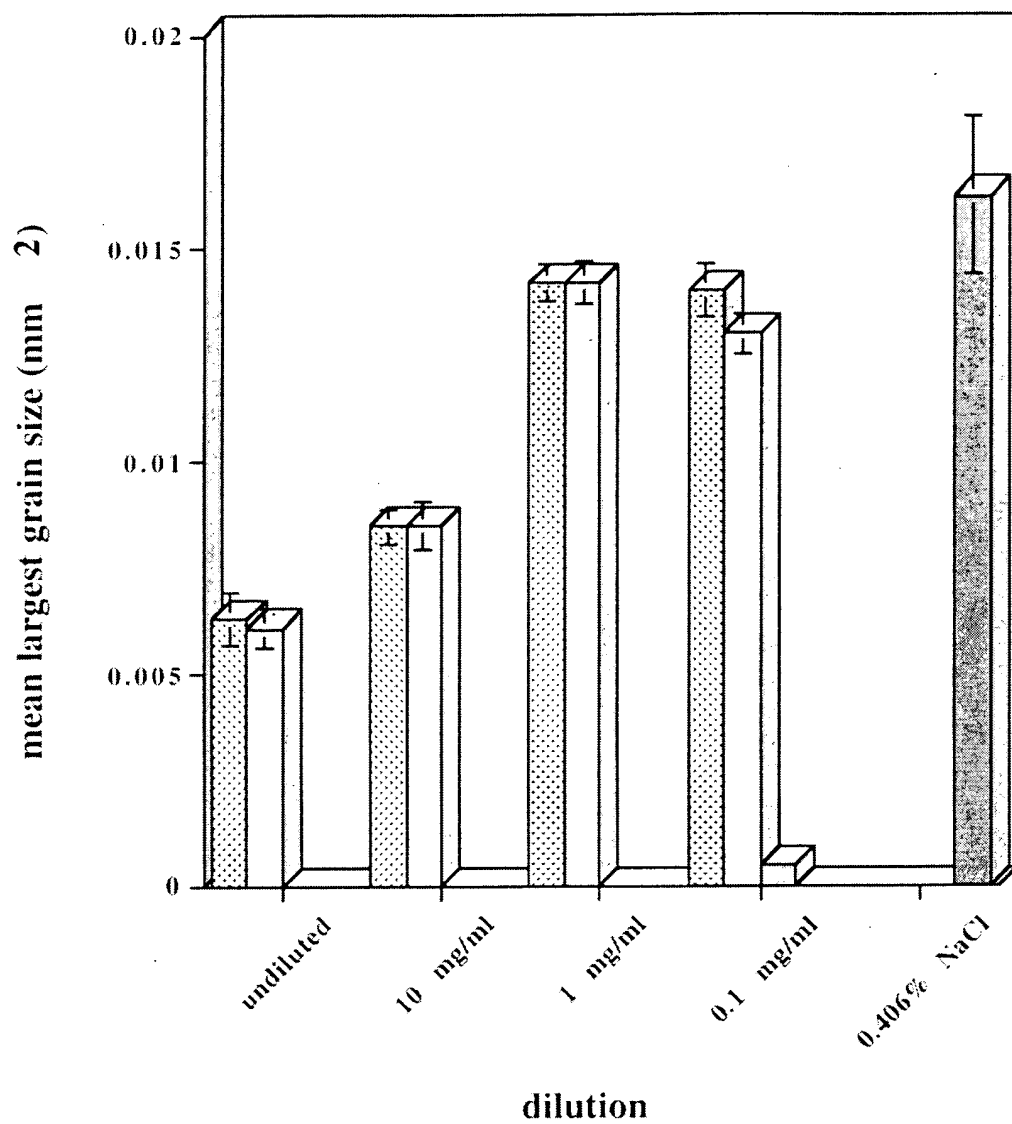


FIG. 8.32

104090-96494860

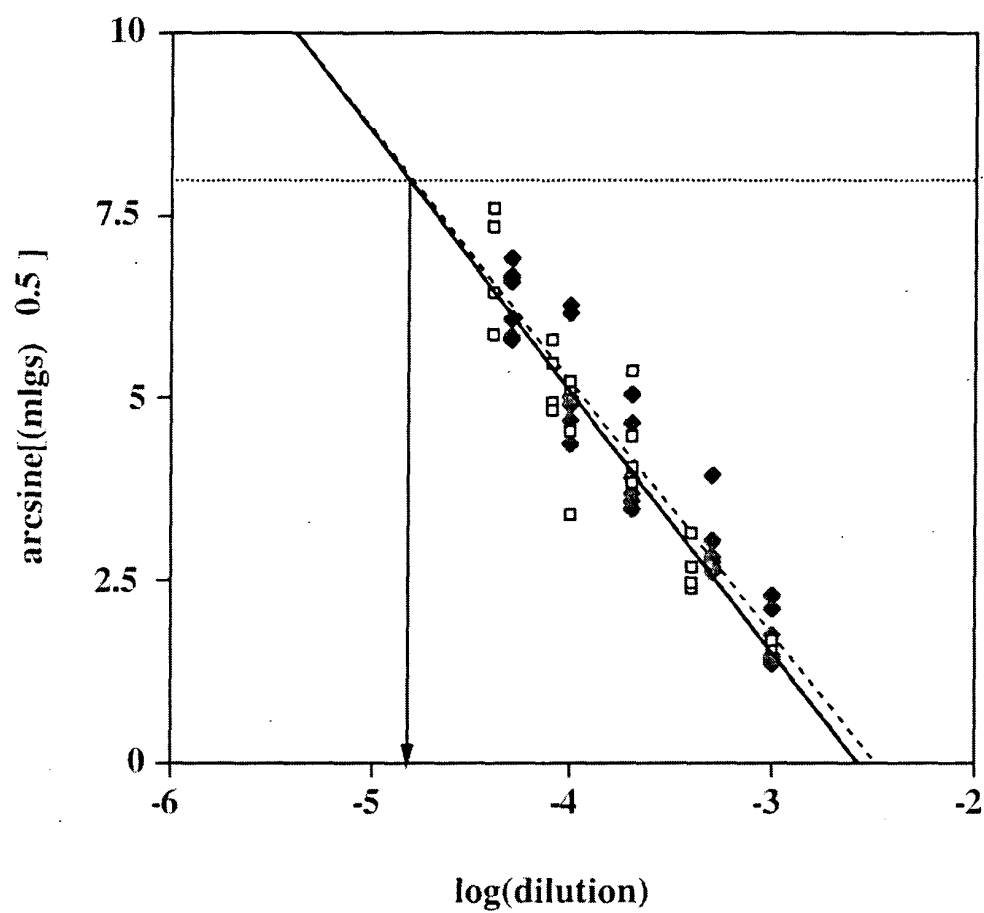


FIG. 8.33

TO2090" 96792860

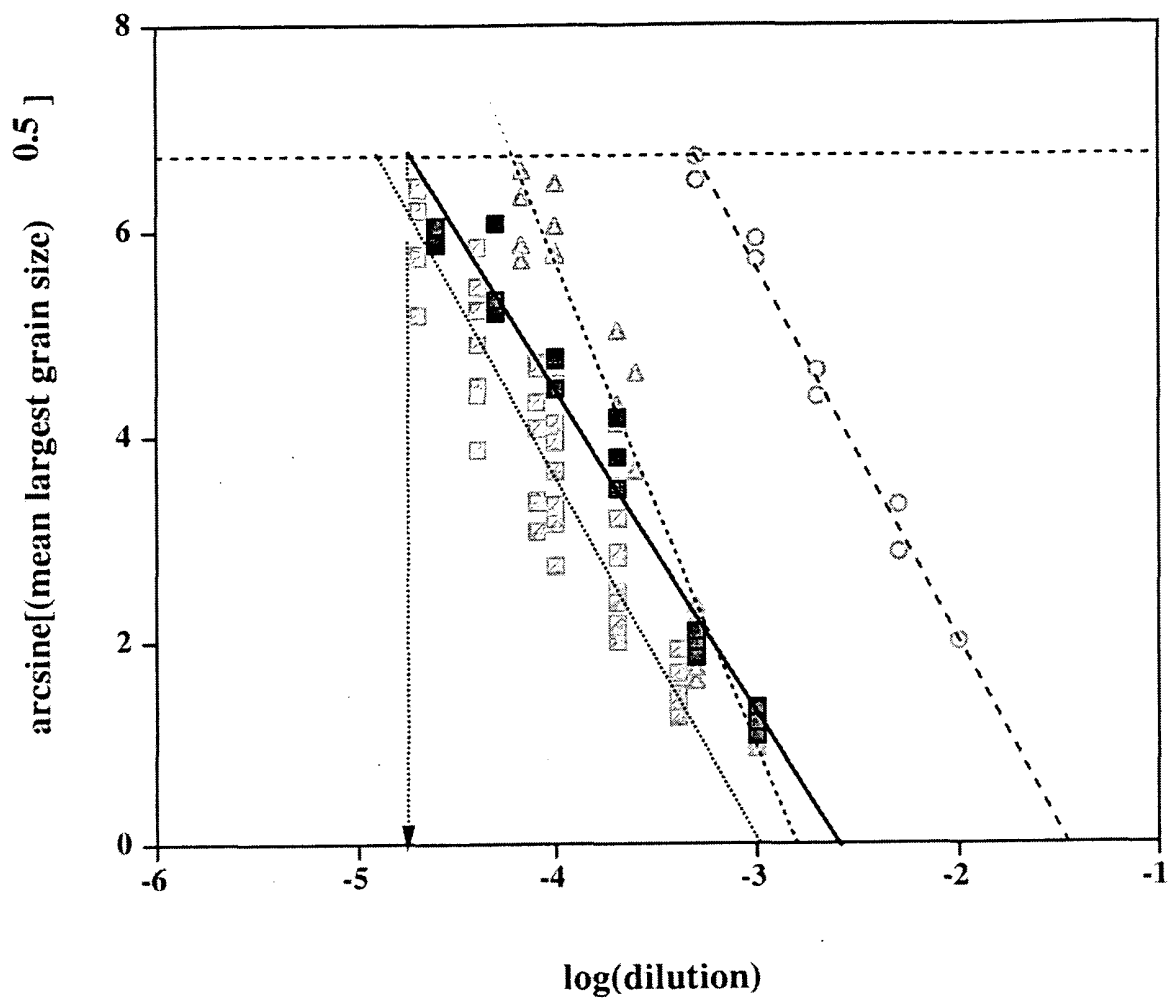


FIG. 8.34

T02090-96/9/860

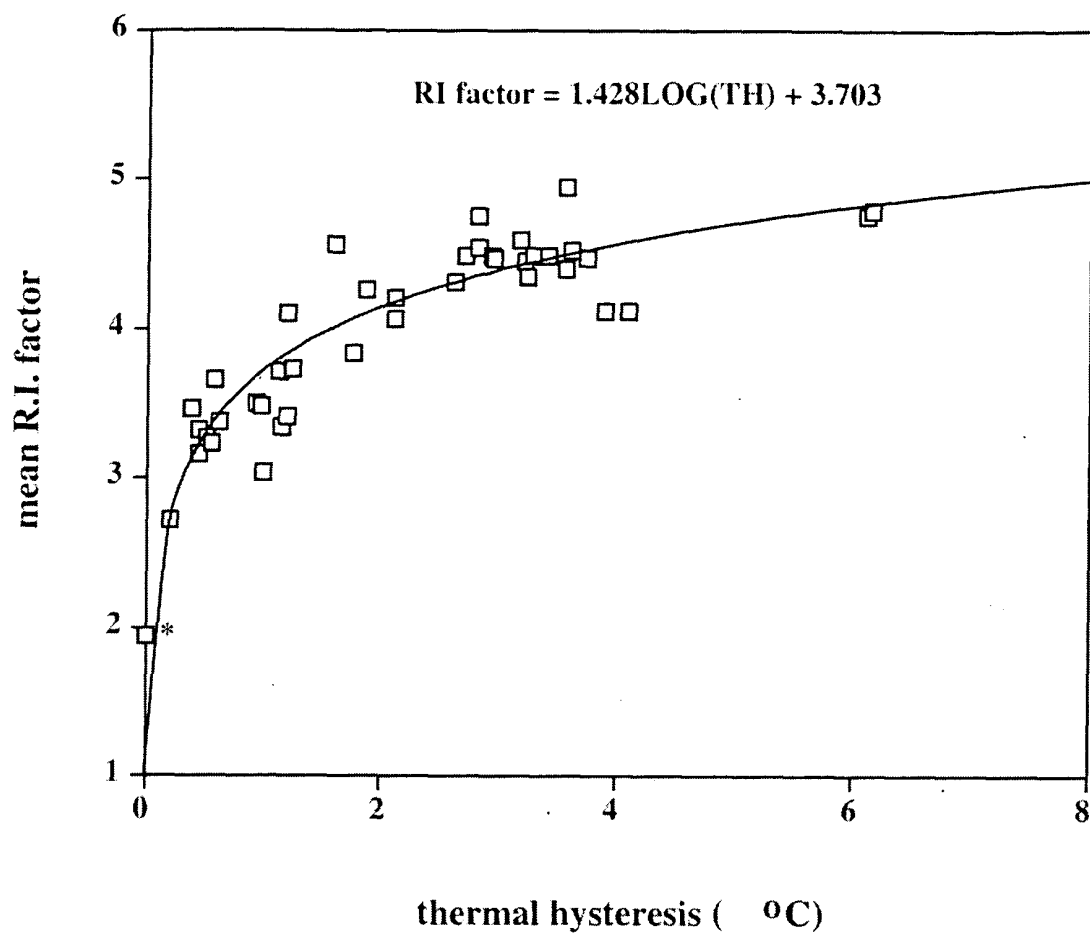


FIG. 8.35

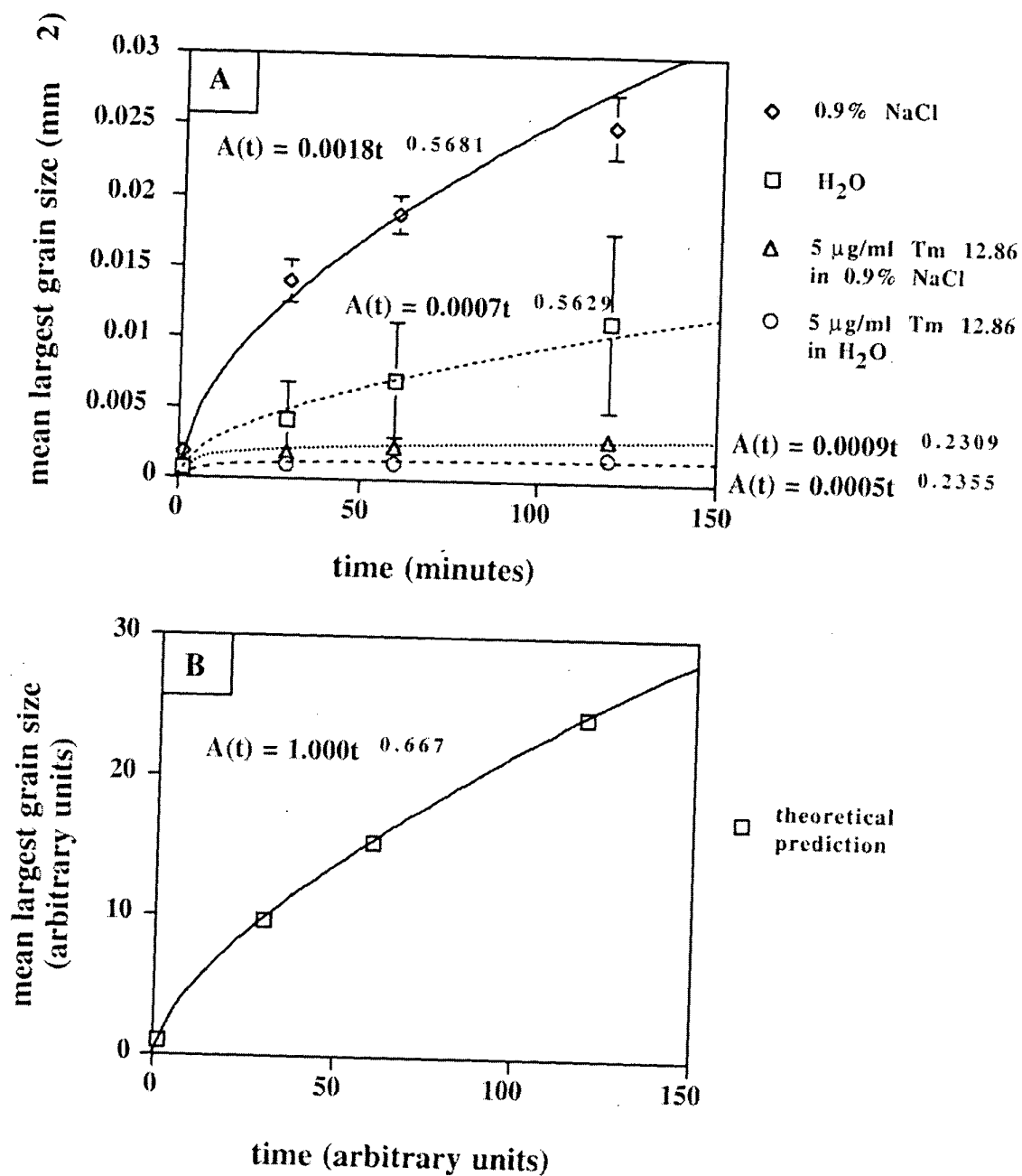


FIG. 8.36

000000-96292860

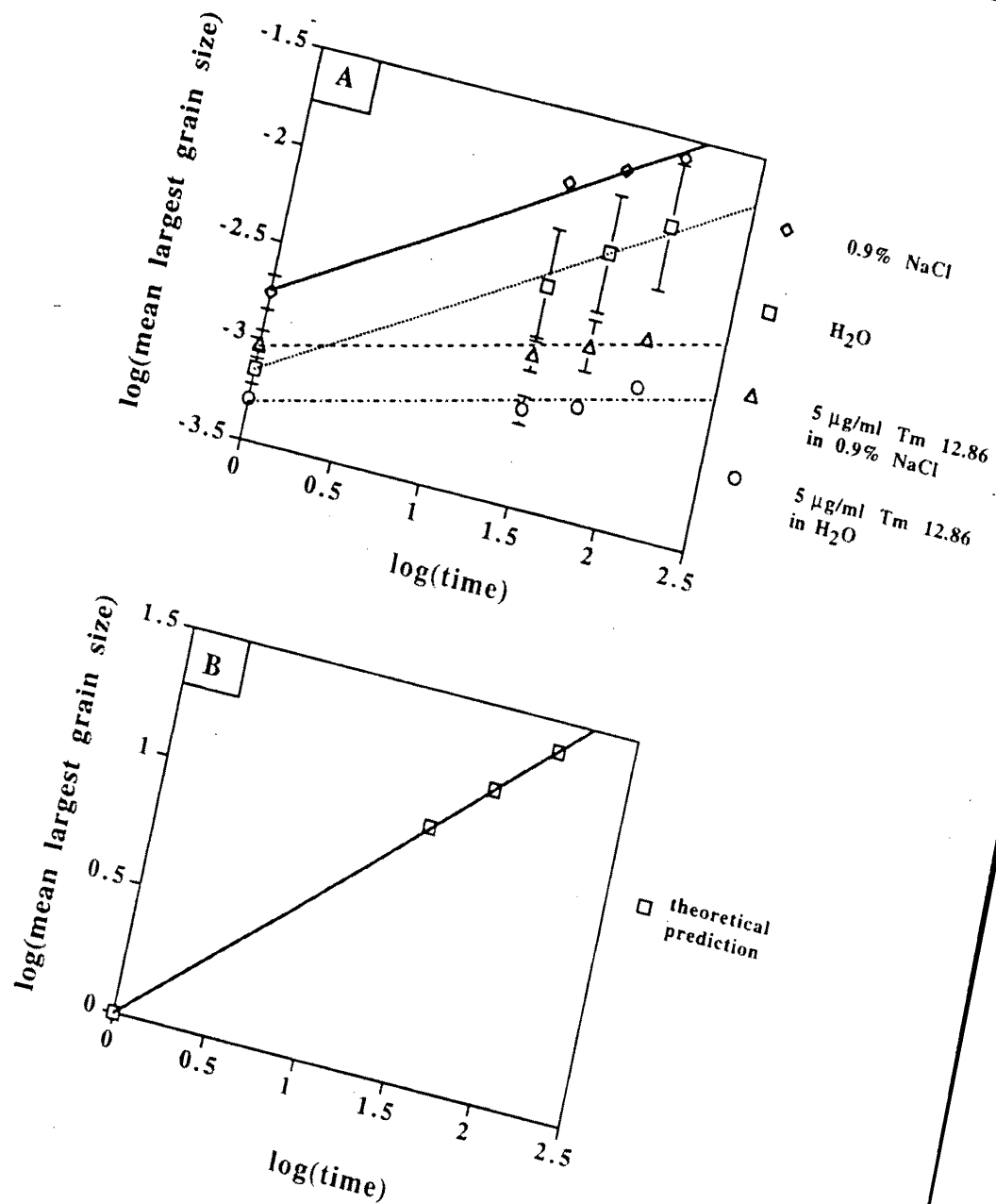
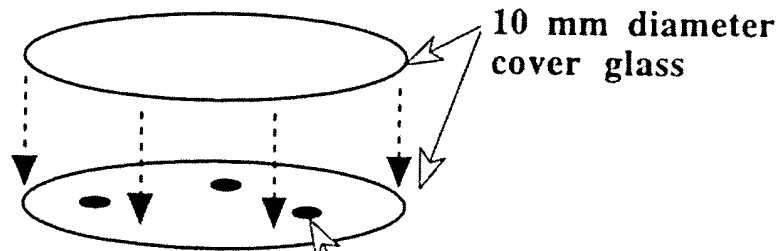


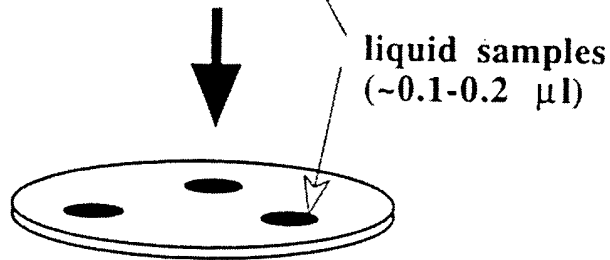
FIG. 8.37

"Sandwich" method of R.I. assessment

1.



2.



3. FREEZE ON ~ -80 C
ALUMINUM PLATE (~10 MIN.)



4. PLACE ON COLD STAGE,
ANNEAL AT -6 C UP TO
12+ HOURS

FIG. 8.38

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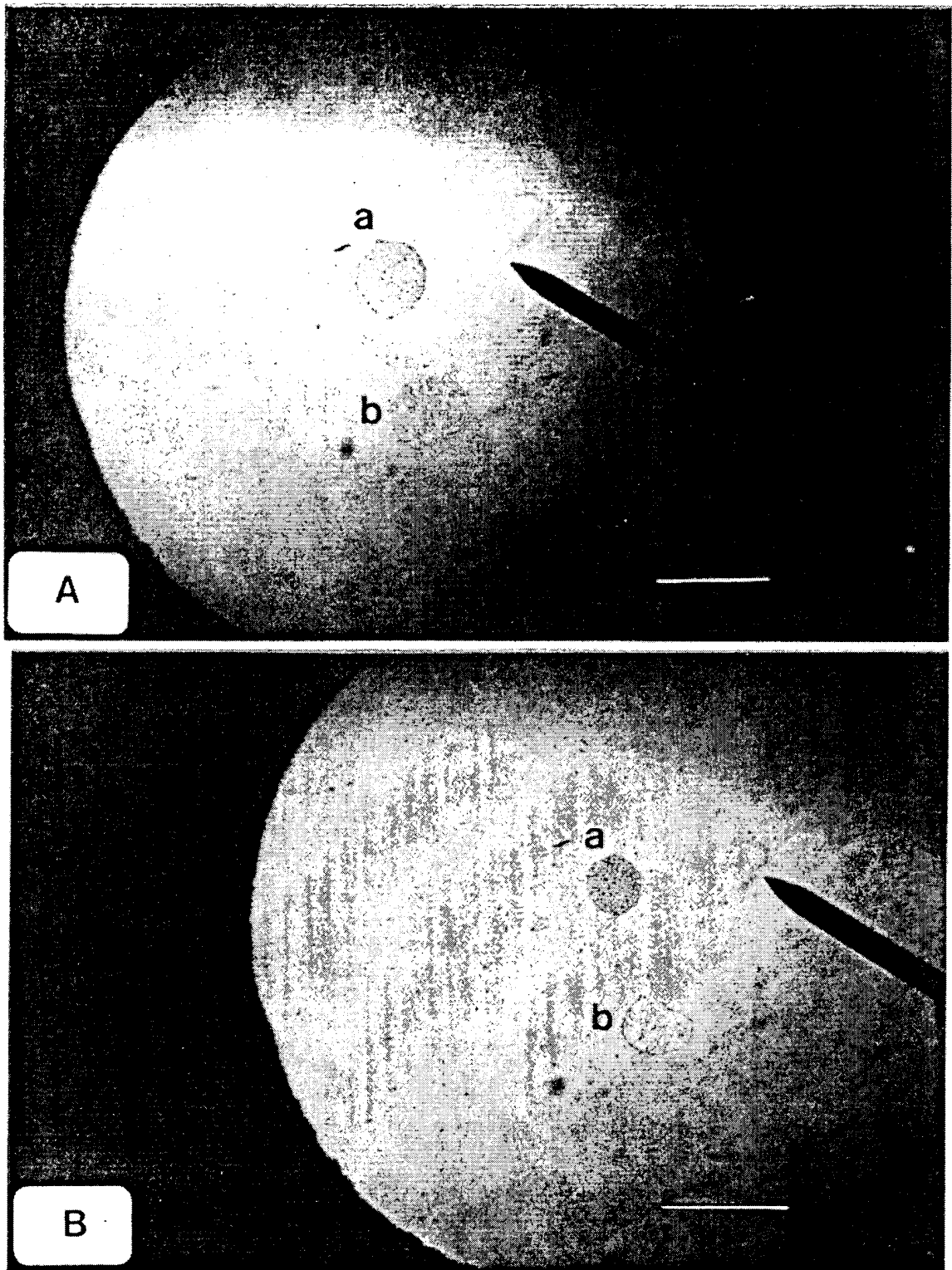


FIG. 8.39

09876796-060701

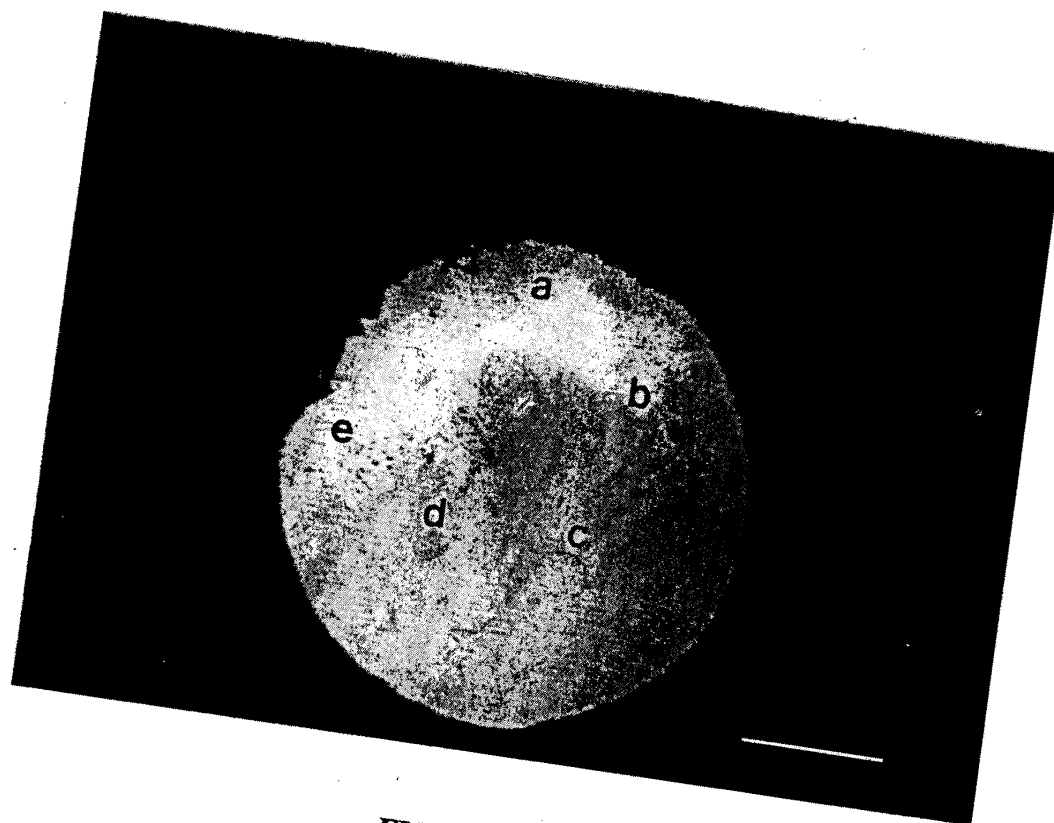


FIG. 8.40

FOI090"96292860

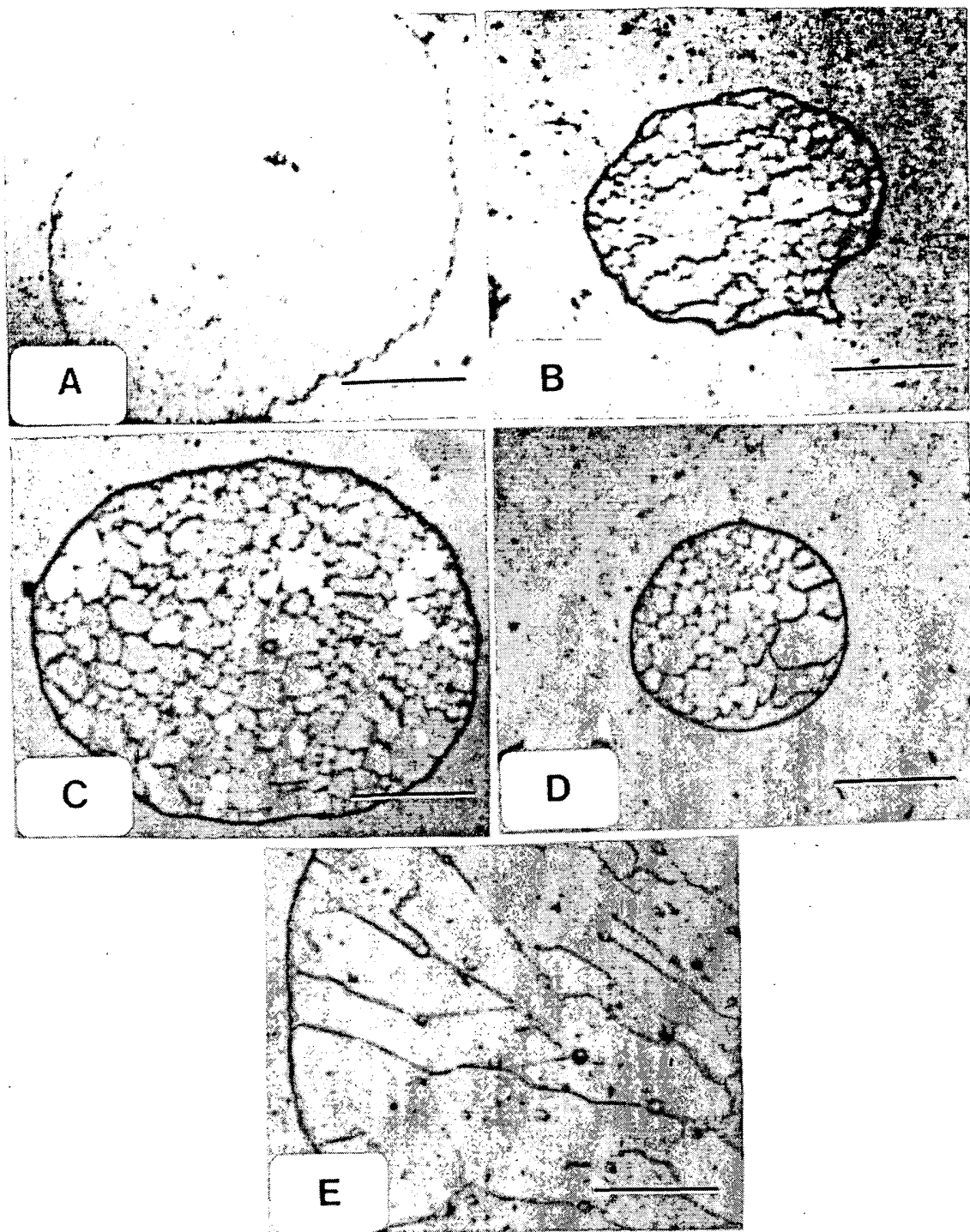


FIG. 8.41

09876795.060701
T07090-96292860

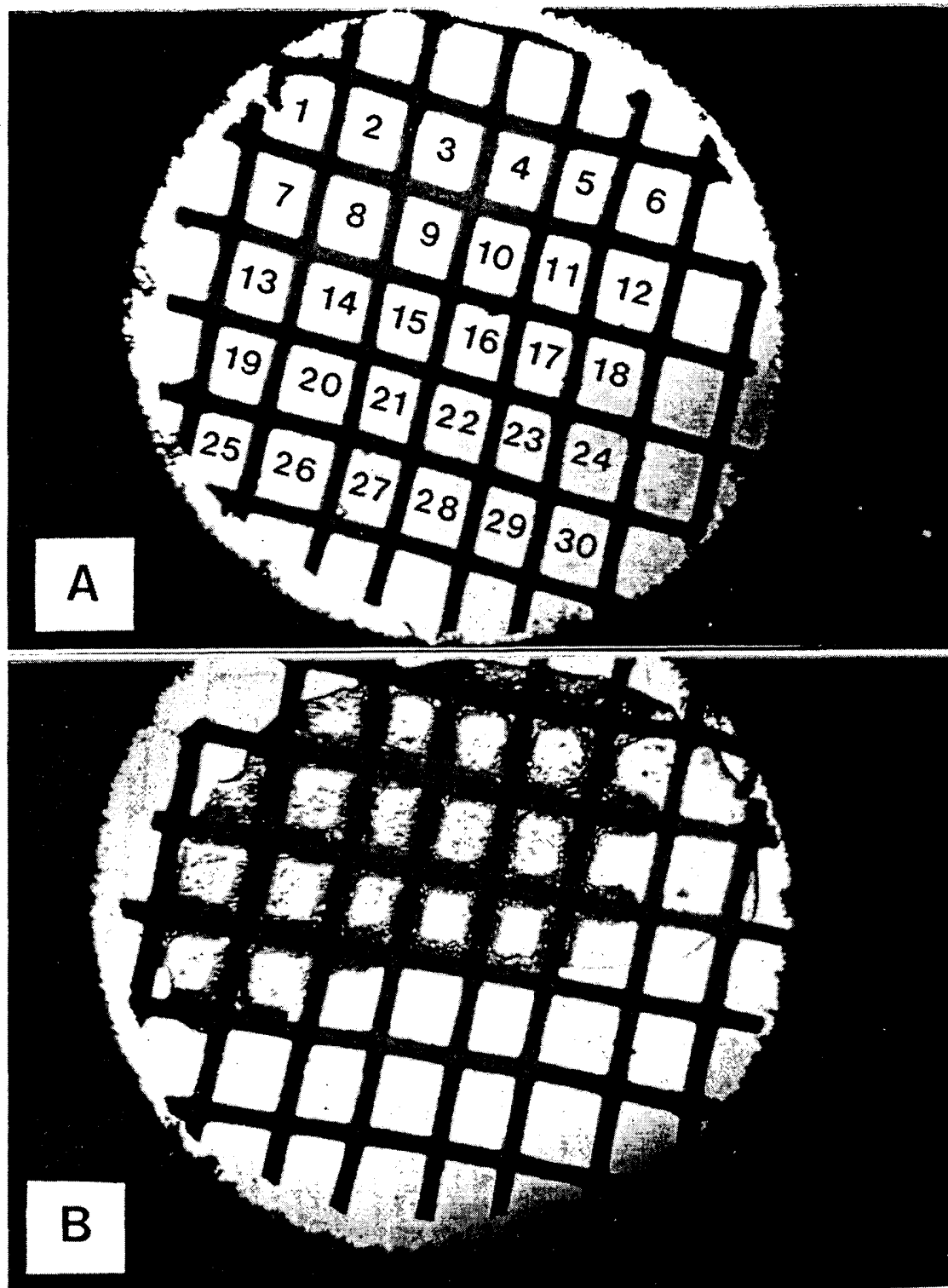


FIG. 8.42

DNA sequence of Tm 13.17 cDNA clone

B E
 a c
 m o
 H R
 I I

1 AGTGGATCCAAAGAATTCGGCACGAGACTACTAAGATGAAGTTGCTCTGTTGTCTAATCT
 M K L L C C L I S

61 CCCTCATTCTGTTGGTCACAGTTCAGGCCCTGACCGAGGCACAAATTGAGAACTGAACA
 L I L L V T V Q A L T E A Q I E K L N K

121 AGATCAGCAAAAAATGTCAAAATGAAAGTGGAGTGTGCGCAAGAGATCATAACCAAAGCTC
 I S K K C Q N E S G V S Q E I I T K A R

181 GCAACGGTGACTGGGAGGACGATCCTAAACTGAAACGCCAAGTTTTTTGCGTGGCCAGGA
 N G D W E D D P K L K R Q V F C V A R N

241 ACGCCGGTCTGGCCACGGAATCGGGAGAGGTGGTGGTCGACGTGTTGAGGGAGAAGGTGA
 A G L A T E S G E V V V D V L R E K V R

301 GGAAGGTCACCTGACAACGACGAAGAACTGAGAAAATCATCAATAAGTGCGCCGTCAAGA
 K V T D N D E E T E K I I N K C A V K R

361 GAGATACTGTTGAAGAGACGGTGTTCATACTTTCAAATGTGTCATGAAAAACAAGCCAA
 D T V E E T V F N T F K C V M K N K P K

421 AGTTCCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC
 F S P V D *

481 ATATAAAATATAAGTGTCTTCTGATGTAAAAAATAAAAAAAAAAAAAAAAAAACTC
 polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

FIG. 8.43

1 GGCACGAGCAAAA ATGAAACTCCTCTTGTGCTTTGCGTTTCGCCGCC
M K L L L C F A F A A

47 ATCGTCATCGGAGCTCAGGCTCTCACCAGACGAACAGATACAGAAA
I V I G A Q A L T D E Q I Q K

92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCC
R N K I S K E C Q Q V S G V S

137 CAAGAGACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D

182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACCTGGA
P K M K K H V L C F S K K T G

226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A

271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V

316 CAGAAGTGCGTGGTCAAGAAGGCCACACCAGAGGAAACGGCTTAT
Q K C V V K K A T P E E T A Y

361 GACACCTTCAAGTGTATTTACGACAGCAAACCTGATTTCTCTCCD
D T F K C I Y D S K P D F S P

406 ATGATTAATTGTTTTGTATTTGACTGAATTTTGACAATAAAGGT
I D

451 ACTATCGTTATGTAAAAAAAAAAAAAAAAAAAAA

polyadenylation signal

poly (A) tail

FIG. 8.44